

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:22 ; Search time 31 Seconds  
(without alignments)  
1008.110 Million cell updates/sec

Title: US-10-743-697-1  
Perfect score: 2046  
Sequence: 1 ELVMTQSPSSLTPTAGEKVT.....LDVWGQGTTLTVSSHHHHH 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCITUS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484.5	72.6	495	2	US-09-948-004-18 Sequence 18, Appl
2	1287.5	62.9	553	1	US-08-263-911-9 Sequence 9, Appl
3	1283	62.7	483	2	US-08-392-338A-19 Sequence 19, Appl
4	1283	62.7	483	2	US-09-166-750-19 Sequence 19, Appl
5	1283	62.7	483	2	US-09-166-093-19 Sequence 19, Appl
6	1283	62.7	483	2	US-09-172-019-19 Sequence 19, Appl
7	1283	62.7	483	2	US-09-166-094-19 Sequence 19, Appl
8	1283	62.7	483	2	US-09-443-213-19 Sequence 19, Appl
9	1230.5	60.1	553	1	US-08-263-911-7 Sequence 7, Appl
10	955	45.7	456	2	US-09-495-880A-11 Sequence 11, Appl
11	938	45.8	249	2	US-09-069-821-2 Sequence 2, Appl
12	938	45.8	249	2	US-09-956-086-2 Sequence 2, Appl
13	938	45.8	249	2	US-09-393-627B-28 Sequence 28, Appl
14	937	45.8	257	2	US-09-420-592A-2 Sequence 2, Appl
15	937	45.8	257	2	US-09-985-442-2 Sequence 2, Appl
16	937	45.8	257	2	US-09-983-580-2 Sequence 2, Appl
17	937	45.8	257	2	US-09-791-540-4 Sequence 4, Appl
18	937	45.8	257	2	US-09-791-540-4 Sequence 4, Appl
19	937	45.8	257	2	US-09-791-540-4 Sequence 4, Appl
20	937	45.8	257	2	US-09-420-592A-4 Sequence 4, Appl
21	937	45.8	269	2	US-09-985-442-4 Sequence 4, Appl
22	937	45.8	269	2	US-09-983-580-4 Sequence 4, Appl
23	937	45.8	269	2	US-09-791-540-6 Sequence 6, Appl
24	937	45.8	269	2	US-09-791-540-6 Sequence 6, Appl
25	937	45.8	269	2	US-09-791-540-6 Sequence 6, Appl
26	937	45.8	269	2	US-08-323-445A-4 Sequence 4, Appl
27	937	45.8	269	2	US-08-323-445A-4 Sequence 4, Appl

28	928.5	45.4	553	1	US-08-661-052-16 Sequence 16, Appl
29	928.5	45.4	553	2	US-09-188-082-16 Sequence 16, Appl
30	928.5	45.4	553	2	US-09-364-088-16 Sequence 16, Appl
31	928.5	45.4	553	2	US-09-102-716-16 Sequence 16, Appl
32	927	45.3	246	2	US-09-791-540-2 Sequence 2, Appl
33	927	45.3	246	2	US-09-791-540-2 Sequence 2, Appl
34	925	45.2	264	1	US-08-323-445A-8 Sequence 8, Appl
35	925	45.2	264	1	US-08-323-445A-8 Sequence 8, Appl
36	925	45.2	264	4	PCT-US95-12840-8 Sequence 8, Appl
37	894.5	43.7	275	2	US-07-935-695-8 Sequence 8, Appl
38	894.5	43.7	275	2	US-07-935-695-8 Sequence 8, Appl
39	890.5	43.5	275	2	US-08-463-903-17 Sequence 17, Appl
40	890.5	43.5	275	2	US-07-935-695-17 Sequence 17, Appl
41	890.5	43.5	280	2	US-08-463-903-10 Sequence 10, Appl
42	890.5	43.5	280	2	US-07-935-695-10 Sequence 10, Appl
43	890.5	43.5	282	2	US-08-463-903-12 Sequence 12, Appl
44	890.5	43.5	282	2	US-08-463-903-15 Sequence 15, Appl
45	890.5	43.5	282	2	US-07-935-695-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1									
US-09-948-004-18									
Sequence 18, Application US/09948004									
Patent No. 6723538									
GENERAL INFORMATION:									
APPLICANT: MACK, Mathias									
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in									
TITLE OF INVENTION: Immunological disorders									
FILE REFERENCE: E 2411 EP									
CURRENT APPLICATION NUMBER: US/09/948,004									
CURRENT FILING DATE: 2001-09-05									
NUMBER OF SEQ ID NOS: 34									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 18									
LENGTH: 495									
TYPE: PRT									
ORGANISM: Mus sp.									
US-09-948-004-18									
Query Match									
Best Local Similarity 74.7% Pred. No. 2.4e-102; Length 495;									
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;									
QY	1	ELVMTQSPSSLTPTAGEKVTMSCKSSQSLNSGNQKNTLTWYQKPGQPKLLIYASTR	60						
DB	1	DIIVLTQSPASLSASVGEFTVITCRASENIY-----SYLAWYQKQKSPOLLVYNAKTL	54						
QY	61	ESGVDPRTFGSGSGTDFITLTSSVQAEIDLAVYYCONDYSYPLTPAGCTYLEIKGGGSGG	120						
DB	55	TGVFSRFSFGSGSGTGFSLKINSILOPEDFGNFCOHYDTPPTFGGTLEIKGGGSGG	114						
QY	121	GGSGGGSGSVOLLESGAEIVRPGTSVSKSCASGAFNTNYMGWVKORPGHLEWIGDI	180						
DB	115	GGSGGGSGSVQ--LQPGAGRVKPGASVSKSCASGYSFISMMNVKORPGGLEWIGDI	173						
QY	181	PGSGNIHNEKFKKATLTADKSSSTAYMOLSLTFEDSAVYFCARLNMDEPDYWGQ	240						
DB	174	HPSDSERTRNQGFRNRAITLVKYSTAVITQSLSPSEDSAVYCYARGEYGIIDYWGQ	233						
QY	241	GTTVTYSSGGGSDIKLQSGAEIARPGASVSKSCASGYSFISMMNVKORPGGLEW	300						
DB	234	GTTVTYSSGGGSDIKLQSGAEIARPGASVSKSCASGYSFISMMNVKORPGGLEW	293						
QY	301	IGYINPSRGTYNNOKFKATLTDDKSSSTAYMOLSLTFEDSAVYFCARYYDDHYC	360						
DB	294	IGYINPSRGTYNNOKFKATLTDDKSSSTAYMOLSLTFEDSAVYFCARYYDDHYC	353						
QY	361	YWGQGTTLTVSS 372							
DB	354	YWRQGTTLTVSS 365							



Db 179 SPGNDFFKYNRFKATLTADKSSSTAYVOLNSLTSEDSAVYFCTRLN---MAYWGQ 234  
Qy 241 GTTVTVSS----- 248  
Db 235 GTSTVSSDVVMSQSPSLPVSVGEKVTLSCKSSQSLISGNQKNYLAAYQKPGQSPKL 294  
Qy 249 -----GGGGSQD----- 254  
Db 295 LIYMASARESGVPDRFTSGSGGTDTFTLSSVKTEDLAIVYCCQYYSYPLTFGAGTKLVL 354  
Qy 255 -----ITLQSGAELAPPGASVKNCSCTSGYTFRTYTMHWKORPGQGL 298  
Db 355 KGSTSGSKSSEBKQVQLQSDALVPRGASVKISCKASGTFTHDAIHWKONPEQGL 414  
Qy 299 EMIGYINPSRGYTNVQKFKKATLTTPDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYC 358  
Db 415 EMIGYFSPGNDFFKYNRFKATLTADKSSSTAYVOLNSLTSEDSAVYFCTRLN---- 470  
Qy 359 LDYWGQGTTLTVS 371  
Db 471 MAYWGQGTSTVYS 483

RESULT 4  
US-09-166-750-19  
Sequence 19, Application US/09166750  
Patent No. 6025165

GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,750  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-166-750-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
Best Local Similarity 53.8%; Pred. No. 2,18-87;  
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

Qy 1 ELVMTQSPSSSLITVAGEKVTMSCKSSQSLNSGNQKNYLYTYYQKPGQPPKLLIYMASTR 60  
Db 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLISGNQKNYLAAYQKPGQSPKLLIYMASAR 60  
Qy 61 ESVGVPDRFPTSGSGGTDTFTLTSVQAEFLAYVYCCNDPSYPLTFGAGTKLEIKGGGSGG 120  
Db 61 ESVGVPDRFPTSGSGGTDTFTLTSVQAEFLAYVYCCNDPSYPLTFGAGTKLVK-GSTSGS 119  
Qy 121 GSGSGGSGSEVOLLRQSGAELVPRGTSYKISCKASGYAFTHYMLGWKORPGHGLEWIDI 180  
Db 120 GKSSEBKQVQ-LQSDALVPRGASVKISCKASGYFTTHDAIHWKONPEGLEWIGYF 178  
Qy 181 FPGSGNIHYNEKFKKATLTADKSSSTAYMQLSLTSEDSAVYPCARLRMDEPYDYGQ 240  
Db 179 SPGNDFFKYNRFKATLTADKSSSTAYVOLNSLTSEDSAVYFCTRLN---MAYWGQ 234  
Qy 241 GTTVTVSS----- 248  
Db 235 GTSTVSSDVVMSQSPSLPVSVGEKVTLSCKSSQSLISGNQKNYLAAYQKPGQSPKL 294  
Qy 249 -----GGGGSQD----- 254  
Db 295 LIYMASARESGVPDRFTSGSGGTDTFTLSSVKTEDLAIVYCCQYYSYPLTFGAGTKLVL 354  
Qy 255 -----ITLQSGAELAPPGASVKNCSCTSGYTFRTYTMHWKORPGQGL 298  
Db 355 KGSTSGSKSSEBKQVQLQSDALVPRGASVKISCKASGTFTHDAIHWKONPEQGL 414  
Qy 299 EMIGYINPSRGYTNVQKFKKATLTTPDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYC 358  
Db 415 EMIGYFSPGNDFFKYNRFKATLTADKSSSTAYVOLNSLTSEDSAVYFCTRLN---- 470  
Qy 359 LDYWGQGTTLTVS 371  
Db 471 MAYWGQGTSTVYS 483

RESULT 5  
US-09-166-093-19  
Sequence 19, Application US/09166093  
Patent No. 6027725

GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,093

FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977,003000B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-166-093-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
Best Local Similarity 53.8%; Pred. No. 2,1e-87;  
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVMTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTMYQOKPQPPKLLIYMASTR 60  
DB 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLYSGNQKNYLAHYQOKPQSPKLLIYMASAR 60  
QY 61 ESVGPRDFTGSGGSDTFTLTISVQAEALVYVYQNDYSYPLTFGAGTKLEIKGGGSGG 120  
DB 61 ESVGPRDFTGSGGSDTFTLTISVQAEALVYVYQNDYSYPLTFGAGTKLVK-GSTSGS 119  
QY 121 GSGSGGSEVQLLEQSAELVPRGTSYKISCKASGYAFTNWLGMVKORPGHLEWIGDI 180  
DB 120 GKSSEGGQVO-LQOSDAELVPRGASVYKISCKASGYFTTDAIHVWKNPQGLEWIGYF 178  
QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRWDEPMYWGQ 240  
DB 179 SPGNDPFKNRFRKATLTADKSSSTAYVQNLSTEDSAVYFCRSLN---MAYWGQ 234  
QY 241 GTTYVSS----- 248  
DB 235 GTSVTSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLYSGNQKNYLAHYQOKPQSPKL 294  
QY 249 -----GGGSD----- 254  
DB 295 LIYMASARESGVPRDFTGSGGSDTFTLTISSVQAEALVYVYQNDYSYPLTFGAGTKLV 354  
QY 255 -----IKLQOSGAELVPRGASVYKISCKASGYFTTRYTMVKNVORPQGL 298  
DB 355 KGTSGSGKSEGGQVO-LQOSDAELVPRGASVYKISCKASGYFTTDAIHVWKNPQGLE 414  
QY 299 EMIGIYNRSRYTNOKFKKATLTADKSSSTAYMQLSLTFEDSAVYFCARLYDDHYC 358  
DB 415 EMWYFSPGNDPFKNRFRKATLTADKSSSTAYVQNLSTEDSAVYFCRSLN--- 470  
QY 359 LDYWGQGTTLTVS 371  
DB 471 MAYWGQGTSTVS 483

RESULT 6  
US-09-172-019-19  
Sequence 19, Application US/09172019  
Patent No. 6103889  
GENERAL INFORMATION:  
APPLICANT: Whitlow, Marc

APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kesler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/172,019  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977,003000D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2540  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-172-019-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
Best Local Similarity 53.8%; Pred. No. 2,1e-87;  
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVMTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTMYQOKPQPPKLLIYMASTR 60  
DB 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLYSGNQKNYLAHYQOKPQSPKLLIYMASAR 60  
QY 61 ESVGPRDFTGSGGSDTFTLTISVQAEALVYVYQNDYSYPLTFGAGTKLEIKGGGSGG 120  
DB 61 ESVGPRDFTGSGGSDTFTLTISVQAEALVYVYQNDYSYPLTFGAGTKLVK-GSTSGS 119  
QY 121 GSGSGGSEVQLLEQSAELVPRGTSYKISCKASGYAFTNWLGMVKORPGHLEWIGDI 180  
DB 120 GKSSEGGQVO-LQOSDAELVPRGASVYKISCKASGYFTTDAIHVWKNPQGLEWIGYF 178  
QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRWDEPMYWGQ 240  
DB 179 SPGNDPFKNRFRKATLTADKSSSTAYVQNLSTEDSAVYFCRSLN---MAYWGQ 234  
QY 241 GTTYVSS----- 248  
DB 235 GTSVTSSDVVMSQSPSSLPVSVGEKVTLSCKSSQSLYSGNQKNYLAHYQOKPQSPKL 294  
QY 249 -----GGGSD----- 254  
DB 295 LIYMASARESGVPRDFTGSGGSDTFTLTISSVQAEALVYVYQNDYSYPLTFGAGTKLV 354

[illegible]

RESULT 7  
US-09-166-094-19  
; Sequence 19, Application US/09166094

APPLICANT: Whitlow, Marc  
APPLICANT: Wood, James F.  
APPLICANT: Hardman, Karl  
APPLICANT: Bird, Robert  
APPLICANT: Filpula, David  
APPLICANT: Rollence, Michelle  
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, NW  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/166,094  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/392,338  
FILING DATE: 22-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/989,846  
FILING DATE: 20-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977.003000A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-166-094-19

Query Match	62.7%	Score 1283;	DB 2;	Length 483;
Best Local Similarity	53.8%	Pred. No. 2.1e-87;		
Matches 265; Conservative	37;	Mismatches 59;	Indels 132;	Gaps 6

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0y 1 ELVMTQSSSLTITAGEKYTMSCSSQSLLNSGNQNYLLTYQKQKQPPKLLIYMASTR 60
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Db	1	DVWMSQSPSSLPVSVGEKVTLSCKSSQSILYSGNQKNYLAWYQQKPGGSPKLLIYMAWSR	60
QY	61	ESGVPRDFTSGSGTDPTLTISISVQAEIDLAVYYCOINDSYLPTFGAGTKLEIKGGGSGG	120
Db	61	ESGVPRDFTSGSGTDPTLTISISVQAEIDLAVYYCOQYISYELTFGAGTKLVK-GSTSGS	119
QY	121	GGSGGGGSEVQLLEQSGAEIVRPGETSVKISCKASGAFNTWLGWYKORPGHGLEWIGDI	180
Db	120	GKSEBKGQQV-LQQSDAEIVKPGASVKISCKASGYTFTDHAIHVMWKQNPBEGLEWIGYF	178
QY	181	FPFGSNIHNANKRFPGKATLTADKSSSTLYMQLSLTFEEDSAVYFCARLRNMDPEMDYMGQ	240
Db	179	SPGNDDEFTYNERFKATLTADKSSSTAYVLQNLSTSEDSAVYFCTRLN---MAYMQG	234
QY	241	GTTVTYSS-----	248
Db	235	GTSVTVSSDVWMSQSPSSLPVSVGEKVTLSCKSSQSILYSGNQKNYLAWYQQKPGGSPKL	294
QY	249	-----GGGGS-----	254
Db	295	LIYMASARESGVPRDFTSGSGGTDFLTLSISVKTEDLAVYYCOQYISYELTFGAGTKLV	354
QY	255	-----IKLQSGAEIARPGASVKMSCKTSGYFTFRYTHMHWYKORPDGGI	298
Db	355	KGSTSGSKSEBKGQQVQLQSDAEIVKPGASVKISCKASGYTFTDHAIHVMWKNPBEGGL	414
QY	299	EWIGIYNSRGYTNYNQFKDKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYDHYC	358
Db	415	EWIGIYNSGNDDEFTYNERFKATLTADKSSSTAYVLNLSLSEDSAVYFCTRLN----	470
QY	359	LDYMGQGTLLTVS 371	
Db	471	MAYMGQGTSTVTS 483	

RESULT 8  
US-09-443-213-19  
; Sequence 19, Application US/09443213

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,936  
FILING DATE: 25-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0977,003000E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-443-213-19

Query Match 62.7%; Score 1283; DB 2; Length 483;  
Best Local Similarity 53.8%; Pred. No. 2,16-87;  
Matches 265; Conservative 37; Mismatches 59; Indels 132; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKXLTWYQKPGQPPKLLIYMASTR 60  
DB 1 DIVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQPPKLLIYMASAR 60  
QY 61 ESVGPRPFTSGSGTDTLTISVQAEIDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120  
DB 61 ESVGPRPFTSGSGTDTLTISVQAEIDLAVYYCONDYSYPLTFGAGTKLVK-GSTRGS 119  
QY 121 GSGSGGSEVQLEBQSGAEIVRPGTSVKISCKASGYAFTNYMLGMVQRPQHGLEWIGDI 180  
DB 120 GKSEBKGQVQ-LQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPQGLEWIGYF 178  
QY 181 FPGSGNIHNEKEFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLNDDEMDYWCQ 240  
DB 179 SPGNDPFRYNERFKGKATLTADKSSSTAYVQNLSTEDSAVYFCSTRSLN---MAYWGG 234  
QY 241 GTTYVSS----- 248  
DB 235 GTSTVTSDDVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQSPKL 294  
QY 249 -----GGGGS----- 254  
DB 295 LIYMASARESGVPDRFTSGSGTDTLTISVQAEIDLAVYYCQYYSYPLTFGAGTKLVL 354  
QY 255 -----IKLQOSGAELARPGASVYMSCTSGYTRTYTMHVQKRPQGL 298  
DB 355 KGSTSGSKSEBKGQVQ-LQOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPQGL 414  
QY 299 EMIGYINPSRGYTNVQKFKATLTADKSSSTAYMQLSLTFEDSAVYFCARYDDHYC 358  
DB 415 EMIGFSPGNDPFRYNERFKGKATLTADKSSSTAYVQNLSTEDSAVYFCSTRSLN---- 470  
QY 359 LDYWGQGTTLTVS 371  
DB 471 MAYWGGTSTVTS 483

RESULT 9  
US-08-263-911-7  
Sequence 7, Application US/08263911  
Patent No. 587291  
GENERAL INFORMATION:  
APPLICANT: Mezes, Peter S  
APPLICANT: Goutille, Brian B  
TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Duane C. Ulmer  
STREET: P.O. Box 1967  
CITY: Midland  
STATE: MI

COUNTRY: US  
ZIP: 48641-1967  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/263,911  
FILING DATE: 21-JUN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,263  
FILING DATE: 11-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ulmer, Duane C  
REGISTRATION NUMBER: 34,941  
REFERENCE/DOCKET NUMBER: C-41,014  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 636-8104  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 23  
US-08-263-911-7

Query Match 60.1%; Score 1230.5; DB 1; Length 553;  
Best Local Similarity 48.3%; Pred. No. 1,9e-83;  
Matches 261; Conservative 37; Mismatches 65; Indels 177; Gaps 6;

QY 1 ELVNTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKXLTWYQKPGQPPKLLIYMASTR 60  
DB 23 DIVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKXLTWYQKPGQSPKL IYMASAR 82  
QY 61 ESVGPRPFTSGSGTDTLTISVQAEIDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120  
DB 83 ESVGPRPFTSGSGTDTLTISVQAEIDLAVYYCONDYSYPLTFGAGTKLVKLSADDAK 142  
QY 121 GSGSGGGS-----EVQLLEQSGAEIVRPGTSVKISCKASGYAFTNYMLGMVQRP 170  
DB 143 KDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAK 201  
QY 171 GHGLEWIGDIFPQSGNIHNEKEFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLN 230  
DB 202 EQGLEWIGYFSPGNDPFRYNERFKGKATLTADKSSSTAYVQNLSTEDSAVYFCSTRSLN 261  
QY 231 WDFEMDYWGQGTYYVSS----- 248  
DB 262 ---MAYWGGTSTVTSLSADDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAKDAK 317  
QY 249 -----GGGGS----- 254  
DB 318 KYTLSCSSQSLNSGNQKXLTWYQKPGQSPKL IYMASARESGVPDRFTSGSGTDTF 377  
QY 255 ----- 254  
DB 378 TLISVQAEIDLAVYYCQYYSYPLTFGAGTKLVKLSADDAKDAKDAKDAKDAKDAKDAK 437  
QY 255 --IKLQOSGAELARPGASVYMSCTSGYTRTYTMHVQKRPQGLEWIGYINPSRGYTN 312  
DB 438 LEVQLOOSDAELVKPGASVKISCKASGYFTDHAIHVWQNPQGLEWIGFSPGNDPFR 497  
QY 313 YNKFQKATLTADKSSSTAYMQLSLTFEDSAVYFCARYDDHYC LDYWGQGTTLTVSS 372  
DB 498 YNERFKATLTADKSSSTAYVQNLSTEDSAVYFCSTRSLN---MAYWGGTSTVTS 553

RESULT 10



NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,086  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977, 2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-956-086-2  
Query Match 45.8%; Score 938; DB 2; Length 249;  
Best Local Similarity 74.0%; Pred. No. 3,8e-62;  
Matches 185; Conservative 23; Mismatches 36; Indels 6; Gaps 3;  
QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKRPQPPKLLIYMASTR 60  
DB 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNTLTWYQKRPQSPKLLIYMASAR 60  
QY 61 ESVGVPDRFTSGSGGTDFLTLSISVOAEDLAVYYCONDYSYPLTFGAGTKLEIKG-GGSG 119  
DB 61 ESVGVPDRFTSGSGGTDFLTLSISVKTEDLAVYYCQYYSYPLTFGAGTKLVKSGTSGSG 120  
QY 120 GGSGGGGSEVQL-LEOSGAEIVRPGTSVKISCKASGAFNTYMLGWVKRPGHLEWIG 178  
DB 121 KPGSGEGSTKQVQLQSGDAELVKGASVKISCKASGTFPTDHAIHVVKQNPBGLEWIG 180  
QY 179 DIPFGSGNIHYNEKFKGKATLTADKSSSTAYVMQSLTFEDSAVYFCARLRNDEPDYV 238  
DB 181 YFSFGNDPFKYNRFGKATLTADKSSSTAYVQNLSTSDSAVYFCRSLN----MAYW 236  
QY 239 GQGTTVTSS 248  
DB 237 GQGTSVTSSN 246

RESULT 13  
US-09-956-087-2  
Sequence 2, Application US/09956087  
Patent No. 674398  
GENERAL INFORMATION:  
APPLICANT: FILPUTA, DAVID

MANG, MAOLIANG  
SHORR, ROBERT  
WHITLOW, MARC  
LEE, LHSYNG S.  
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS  
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/956,087  
FILING DATE: 20-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/069,821  
FILING DATE: 1998-04-30  
APPLICATION NUMBER: US 60/063,074  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: US 60/050,472  
FILING DATE: 23-JUN-1997  
APPLICATION NUMBER: US 60/044,449  
FILING DATE: 30-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 0977, 2280003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 249 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-956-087-2  
Query Match 45.8%; Score 938; DB 2; Length 249;  
Best Local Similarity 74.0%; Pred. No. 3,8e-62;  
Matches 185; Conservative 23; Mismatches 36; Indels 6; Gaps 3;  
QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKRPQPPKLLIYMASTR 60  
DB 1 DVVMSQSPSSLPVSVGEKVTLSCKSSQSLNSGNQKNTLTWYQKRPQSPKLLIYMASAR 60  
QY 61 ESVGVPDRFTSGSGGTDFLTLSISVOAEDLAVYYCONDYSYPLTFGAGTKLEIKG-GGSG 119  
DB 61 ESVGVPDRFTSGSGGTDFLTLSISVKTEDLAVYYCQYYSYPLTFGAGTKLVKSGTSGSG 120  
QY 120 GGSGGGGSEVQL-LEOSGAEIVRPGTSVKISCKASGAFNTYMLGWVKRPGHLEWIG 178  
DB 121 KPGSGEGSTKQVQLQSGDAELVKGASVKISCKASGTFPTDHAIHVVKQNPBGLEWIG 180  
QY 179 DIPFGSGNIHYNEKFKGKATLTADKSSSTAYVMQSLTFEDSAVYFCARLRNDEPDYV 238  
DB 181 YFSFGNDPFKYNRFGKATLTADKSSSTAYVQNLSTSDSAVYFCRSLN----MAYW 236  
QY 239 GQGTTVTSS 248  
DB 237 GQGTSVTSSN 246

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RESULT 14
US-09-393-627B-28
; Sequence 28, Application US/09393627B
; Patent No. 6455314
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovacs, Imre
; APPLICANT: Roelink, Petrus W.
; APPLICANT: Bruder, Joseph T.
; TITLE OF INVENTION: Alternatively Targeted Adenovirus
; FILE REFERENCE: 202345
; CURRENT APPLICATION NUMBER: US/09/393,627B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,851
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 60/136,529
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent Ver. 2.2
; SEQ ID NO 28
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Anti-HA ScFv fused in frame with 2 C-terminal myc epitopes and
; PDGF receptor transmembrane anchor (Anti-HA pseudo-receptor)
US-09-393-627B-28

Query Match 45.8%; Score 938; DB 2; Length 354;
Best Local Similarity 71.3%; Pred. No. 5.8e-62;
Matches 179; Conservative 28; Mismatches 40; Indels 4; Gaps 3;

QY 1 ELVMTQSPSSSLTVTAGEKVTWCKSSQSLINSGNQKNTLTWYQKPGQPKLLIYMASTR 60
DB 27 DIVMTQSPSSSLTVTAGEKVTWCKSSQSLINSGNQKNTLTWYQKPGQPKLLIYMASTR 86
QY 61 ESGVDRFTGSGGSDFTLTSSVQADLAIVYCCQNDYSYPLTFGAGTKLEIKG-GGGGS 118
DB 87 ESGVDRFTGSGGSDFTLTSSVQADLAIVYCCQNDYSYPLTFGAGTKLEIKRAAGGGS 146
QY 119 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWVKORPGHLEWIG 178
DB 147 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWVKORPGHLEWVP 205
QY 179 DIPGSGNIHYNKPKKATLTADKSSSTAYVQSLTFEDSAVYFCARLRNMDP-MDY 237
DB 206 TIIRGSGYTYYPDSYGRFTISKNNAKNTLYLQMSLSKSDYAMYYCARETFDEKGFAY 265
QY 238 WGGTITVTVSS 248
DB 266 WGGTITVTVSA 276

RESULT 15
US-09-420-592A-2
; Sequence 2, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Mang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CC49/218 scFv

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US-09-420-592A-2

Query Match 45.8%; Score 937; DB 2; Length 257;
Best Local Similarity 74.3%; Pred. No. 4.7e-62;
Matches 185; Conservative 22; Mismatches 36; Indels 6; Gaps 3;

QY 1 ELVMTQSPSSSLTVTAGEKVTWCKSSQSLINSGNQKNTLTWYQKPGQPKLLIYMASTR 60
DB 1 DIVMTQSPSSSLTVTAGEKVTWCKSSQSLINSGNQKNTLTWYQKPGQPKLLIYMASTR 60
QY 61 ESGVDRFTGSGGSDFTLTSSVQADLAIVYCCQNDYSYPLTFGAGTKLEIKG-GGGG 119
DB 61 ESGVDRFTGSGGSDFTLTSSVQADLAIVYCCQNDYSYPLTFGAGTKLEIKSGSGG 120
QY 120 GGGSGGGGSEVQLLEQSGAEIVRPQTSYKISCKASGYAFITNYMLGWVKORPGHLEWIG 178
DB 121 KPGSGEGSTKQVQLQDSGAEIVRPQTSYKISCKASGYAFITDHAHWKQNPQGLEWIG 180
QY 179 DIPGSGNIHYNKPKKATLTADKSSSTAYVQSLTFEDSAVYFCARLRNMDPMDY 238
DB 181 YFSPENDDFKYNKPKKATLTADKSSSTAYVQSLTFEDSAVYFCARLRNMDPMDY 236
QY 239 GGGTITVTVS 247
DB 237 GGGTITVTVS 245

Search completed: March 6, 2006, 13:14:16
Job time : 32 secs

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A:Molecule type: mRNA  
A:Residues: 1-113 <SHL>  
A:Cross-references: UNIPARC:UPI0000176AF7  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-96/Domain: immunoglobulin homology <IMM>  
F:24-40/Region: complementarity-determining 1  
F:41-55/Region: complementarity-determining 2  
F:56-62/Region: complementarity-determining 2  
F:63-94/Region: framework 3  
F:95-103/Region: complementarity-determining 3  
F:104-113/Region: framework 4

Query Match 28.2%; Score 576; DB 2; Length 113;  
Best Local Similarity 96.5%; Pred. No. 1.9e-30;  
Matches 109; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK 113  
Db 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK 113

RESULT 3  
A31790  
Ig kappa chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C/Accession: A31790  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti-  
A:Reference number: A92686; MUID:89034213; PMID:3182835  
A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:G533234; PIRN:AAA38  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 27.5%; Score 563.5; DB 2; Length 220;  
Best Local Similarity 52.3%; Pred. No. 2.5e-29;  
Matches 123; Conservative 19; Mismatches 48; Indels 45; Gaps 5;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEIKGGGSGG 120  
Db 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEIK----- 113

Qy 121 GSGSGGSEVQLLESGAEIVRPGTSVKISCKAGYATNWLGMVKRPHGLEMIGDI 180  
Db 114 --RADAPTVSIFPPSSSQTLSGASV-----VCFLNLF 145

Qy 181 PPGSGNIHY---NEKFKGATLTADK--SSSTAVYQQLSLT-----FEDSAVYFC 225  
Db 146 YPKDINVMKIDGSEKGVNLSWTDQDSKDYTSMSSTLTLTLDYERHNSYTC 200

RESULT 4  
F30538  
Ig kappa chain V region (253.15D10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C/Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 21-Jan-2000  
C/Accession: F30538  
R:Claflin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum  
A:Reference number: A30534; MUID:89035545; PMID:3141511  
A:Accession: F30538  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-112 <CLA>  
A:Cross-references: UNIPARC:UPI0000176CD5  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 548; DB 2; Length 112;  
Best Local Similarity 92.9%; Pred. No. 1.1e-28;  
Matches 104; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVWTGSPSSLTVSAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYGASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEI 112  
Db 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDHSYPLTFGAGTKLEI 112

RESULT 5  
E30538  
Ig kappa chain V region (253.12D3) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C/Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 21-Jan-2000  
C/Accession: E30538  
R:Claflin, J.L.; Berry, J.  
J. Immunol. 141, 4012-4019, 1988  
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneum  
A:Reference number: A30534; MUID:89035545; PMID:3141511  
A:Accession: E30538  
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-112 <CLA>  
A:Cross-references: UNIPARC:UPI0000176CD4  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 26.6%; Score 545; DB 2; Length 112;  
Best Local Similarity 92.0%; Pred. No. 1.8e-28;  
Matches 103; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELVWTGSPSSLTVTAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVWTGSPSSLTVSAGEKVTMSCKSSQSGLNSGNQKXYLTWYQKPGQPPKLLIYGASTR 60

Qy 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDYSYPLTFGAGTKLEI 112  
Db 61 ESGVPRFTGSGSGTDFTLTITSSVQAEADLAIVYCCNDHSYPLTFGAGTKLEI 112

RESULT 6  
PL0264  
Ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C/Accession: PL0264  
R:Shlomchik, M.; Macceilli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic m  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0264  
A:Molecule type: mRNA  
A:Residues: 1-113 <SHL>  
A:Cross-references: UNIPARC:UPI0000176AFB  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin



```
0Y      1 ELVMTSPSSLLVTAGEKYTMSCKSSQSLNSGNKNYLTYOQRGQPPLKLIYMASTR 6
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Db 123 GGGGGDSSGGGGSDIELTQSPALMSASLGEKVTMSCRASSVNF-----IYWYQKSDASP 178



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Db 175 SITSGYMWIRKPFKPKLDYWGVI-NYSGDYNNPSLSKRISITADTSKNQYQLNLSVT 233  
Qy 217 FEDSAVYFC-ARLNMDEPMDYWGQGTYYVSS 248  
Db 234 TEDATATYCGGGGLRT---MDYWGQGTYSIVSS 262

## RESULT 2

07TQM2\_MOUSE PRELIMINARY; PRT; 243 AA.  
ID 07TQM2\_MOUSE PRELIMINARY; PRT; 243 AA.  
AC 07TQM2\_MOUSE PRELIMINARY; PRT; 243 AA.  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE scfv 6H8 protein (Fragment).  
GN Name=scfv 6H8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c;  
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;  
RA Peter J.C., Eftekhari P., Billiard P., Mailukat G., Hoebecke J.;  
RT "scfv single chain antibody variable fragment as inverse agonist for  
the beta-2 adrenergic receptor."  
RL J. Biol. Chem. 278:36740-36747(2003).  
DR EMBL; AJ574851; CAB00495.1; -; Genomlc\_DNA.  
DR HSSP; P01751; 1A6W.  
DR SMR; 07TQM2; 1-236.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1  
SQ SEQUENCE 243 AA; 25976 MW; B6FF64D2DCFAF76 CRC64;

Query Match 27.7%; Score 566; DB 2; Length 243;  
Best Local Similarity 47.0%; Pred. No. 1.9e-34;  
Matches 124; Conservative 33; Mismatches 71; Indels 36; Gaps 9;  
Qy 129 EVOLLESGAEVLVPGTSTVSKSCASGYAFNNYMGWVKORPGHLEWIGIPFGSGNIIH 188  
Db 1 QVQ-LQSGSGLVPRGASVSKSCASGYFTFTTMMWVKQKHGQLEWIGIYFSGSITN 59  
Qy 189 YNEKFKGKATLTADKSSSTAYMOLSLTFEDSAVYFCARLNMDEPMDYWGQGTYYVS- 247  
Db 60 YDEKFKNGKILTVDTSSSTAYMHLSSLASDSAVYYCAR---GGRGLDVGAGTTLTVSS 116  
Qy 248 -----SGGGSDILQOGSAGELA-RPGASVYMSCKTGYFTTMMWVKORPGQG 297  
Db 117 GGGSGGGSGGGSDIDMTSSSFVSLDRLVITTCASEDIYNN--LAWYQOKP-- 172  
Qy 298 LEWIGIYNSR---GYNNYQKFKDKATLTLDKSSSTAYMOLSLTFEDSAVYFCARY 353  
Db 173 -----NAPRLLSGATSLSTGVPSR--FGSGSGKDYTLSTSLQTEDAIYYICQY 223  
Qy 354 DDHYCLDYWGQGTTLTVSSHHNH 377  
Db 224 STR-----TFGGGTKEIKHHNH 243

RESULT 3  
Q6KB05\_MOUSE PRELIMINARY; PRT; 255 AA.  
ID Q6KB05\_MOUSE PRELIMINARY; PRT; 255 AA.  
AC Q6KB05\_MOUSE PRELIMINARY; PRT; 255 AA.  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE scfv B8E5 protein (Fragment).  
GN Name=scfv B8E5;

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c;  
RA Peter J.C., Mailukat G., Tugler J., Maurice D., Roegel J.C.,  
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with  
monoclonal anti-M2 receptor antibody fragments."  
RL J. Biol. Chem. 279:55697-55706(2004).  
DR EMBL; AJ746180; CAG34081.1; -; Other\_DNA.  
DR HSSP; P01837; 1KCR.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON TER 1  
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 25.8%; Score 528; DB 2; Length 255;  
Best Local Similarity 90.3%; Pred. No. 1.5e-31;  
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ELVMTQSPSSLTYYAGKVTMSCKSSQSLNSGNQKYYLWYQOKPQPPKLLIYMASTR 60  
Db 137 DIVMAQSPSSLSVAGKVTMSCKSSQSLNSRNQKYYLWYQOKPQSPKLLIYGASTR 196  
Qy 61 ESGVPRFTSGSGTDTLTITSSVQAEFLAVYCONDYVPLFGAGTKLEIK 113  
Db 197 ESGVPRFTSGSGTDTLTITSSVQAEFLAVYCONDYVPLFGAGTKLEIK 249

## RESULT 4

09GY22\_MOUSE PRELIMINARY; PRT; 119 AA.  
ID 09GY22\_MOUSE PRELIMINARY; PRT; 119 AA.  
AC 09GY22\_MOUSE PRELIMINARY; PRT; 119 AA.  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy  
chain variable region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Song X.T., Peng Z.Q., Guan X.H.;  
RT "Amplification, cloning and sequence analysis of the heavy chain  
variable region gene of monoclonal anti-idiotypic antibody NP30 of  
Schistosoma japonicum";  
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF282622; AA01452.1; -; mRNA.  
DR EMBL; AF282622; AA01452.1; -; mRNA.  
DR HSSP; P01751; 1A6W.  
DR SMR; 09GY22; 1-119.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON TER 1  
SQ SEQUENCE 119 AA; 11967 MW; BA893873FDSFA6AB CRC64;

Query Match 25.8%; Score 527; DB 2; Length 119;  
Best Local Similarity 78.8%; Pred. No. 6.8e-32;  
Matches 93; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 255 IKLQSGAELARPGASVYMSCKTSGYTFRTYTMWVKORPGQGLEWIGYINPSRGYTN 314  
 Db 2 VOLVESGAELVKKPGASVYVSCSKASGYTFRTYTMWVKORPGQGLEWIGYINPSRGYTN 61  
 QY 315 OKFQDKATLTLDKSSSTAYMQLSLTSEDSAVVYCARVDHYGLDPMWQGTLLTVSS 372  
 Db 62 OKFQDRVMTTDSFSTAYMDLRSLRSADSAVYICARYDDHYCLDPMWQGTLLTVSS 119

RESULT 5

Q4KML5\_MOUSE PRELIMINARY; PRT; 617 AA.

AC Q4KML5;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

NUCLEOTIDE SEQUENCE.

RA STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
 RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marubina K., Farmer A.F., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,  
 RA Richards S., Wozniak K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Wozniak K.C., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC098504; AAH98504.1; -; mRNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;

Query Match 25.6%; Score 524.5; DB 2; Length 617;  
 Best Local Similarity 78.7%; Pred. No. 8e-31;  
 Matches 100; Conservative 9; Mismatches 13; Indels 5; Gaps 2;

QY 250 GGGSDIKLQSGAELARPGASVYMSCKTSGYTFRTYTMWVKORPGQGLEWIGYINPSRG 309  
 Db 16 GVHSGVQLQSGAELAKPGASVYVLSCKASGYTFRTYTMWVKORPGQGLEWIGYINPSRG 75  
 QY 310 YNNYNNKFKDKATLTLDKSSSTAYMQLSLTSEDSAVVYCARVDHYGLDPMWQGTLLTVSS 365  
 Db 76 YTKYNNKFKDKATLTLDKSSSTAYMQLSLTSEDSAVYICAR-REGHLMLVYAMDYWGQ 134  
 QY 366 TLLTVSS 372  
 Db 135 TSVTVSS 141

RESULT 6

065ZL2\_9MURI PRELIMINARY; PRT; 487 AA.

AC 065ZL2;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE FV/M4.  
 GN Name=M4-IFN- $\epsilon$ -tau>;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;

NUCLEOTIDE SEQUENCE.

RA QI Y., Xiang J.;  
 RA "A genetically engineered single-gene-encoded anti-TAG72 chimeric  
 RT antibody secreted from myeloma cells."  
 RL Hum. Antibodies Hybridomas 6:161-166(1995).  
 DR EMBL; S82493; AAB37424.2; -; mRNA.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003598; IG-c2.  
 DR InterPro; IPR003006; IG-MHC.  
 DR InterPro; IPR003596; IG-V.  
 DR Pfam; PF07654; CI-sect; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR SMART; SM00408; IGC2; 2.  
 DR SMART; SM00406; IGV; 2.  
 DR PROSITE; PS50835; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG-MHC; 1.  
 SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 25.3%; Score 518; DB 2; Length 487;  
 Best Local Similarity 46.2%; Pred. No. 1.8e-30;  
 Matches 122; Conservative 35; Mismatches 63; Indels 44; Gaps 9;

QY 125 GGGSEVQLQSGAELARPGASVYMSCKTSGYTFRTYTMWVKORPGQGLEWIGYINPSRG 184  
 Db 16 GVHSGVQLQSGDAELVPGASVYVLSCKASGYTFRTYTMWVKORPGQGLEWIGYINPSRG 74  
 QY 185 GNHYNEKFKDKATLTLDKSSSTAYMQLSLTSEDSAVVYICARLRLNWDPMYDQGTTV 244  
 Db 75 DDIKNEKFKDKATLTLDKSSSTAYMQLSLTSEDSAVVYICARLRLNWDPMYDQGTTV 129  
 QY 245 TVSS-----SGGGSDIKLQSGAELARPGASVYMSCKTSGYTFRTYTMWVKORPG 294  
 Db 130 TSSGGGSGGGSGGGSGGSRIGWTQSPASIVSGLVYITCAASNNYS--NLAWYQDQ 187  
 QY 255 GQGLEWIGYIN-----PSRGYTNVYNNKFKDKATLTLDKSSSTAYMQLSLTSEDSAV 346  
 Db 188 GSPDLVLYAATNLADGVPSR-----FSGSGSGTQYSLKINLSQSDPFS 232  
 QY 347 YVCARYDDHYCLDPMWQGTLLTV 370  
 Db 233 YTCQHFVWGPYR---FGGTRLEI 253

RESULT 7

052L64\_MOUSE PRELIMINARY; PRT; 240 AA.

AC 052L64;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RX MDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N;  
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC094049; AAH94049.1; -, mRNA.  
DR SNR: Q52641; 21-240.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF07654; Cl-sect; 1.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGcl; 1.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 26609 MW; CF8630CCC02E52C CRC64;  
Query Match 24.9%; Score 508.5; DB 2; Length 240;  
Best Local Similarity 47.7%; Pred. No. 4e-30;  
Matches 112; Conservative 26; Mismatches 52; Indels 45; Gaps 5;  
QY 1 ELVNTGSPSSLTVTAGEKVTWSCSSQSLNSGNKNTLYTQKPPQPKLLIYMASTR 60  
DB 21 DIVASQSSSLAVSGEKVTWSCSSQSLLYSYNKNLYAQQKPGQSPKLLIYMASTR 80  
QY 61 ESGVDPRTTSGSGGDFLTLTSSVQAEALVYVCONDSVLTGAGKLEIKGGGSGG 120  
DB 81 ESGVDPDHSQSGSGGDFLTLTSSVQAEALVYVCOQYNNYPLTGTGAGTKDLR----- 133  
QY 121 GSGGSGSEVOLLEQSGAEIVRPGTSVKISCKASGYAFNTYMLGWKORPGHGLEWIGDI 180  
DB 134 --RDAATVTSIFPSSSQLTSGASV-----VCFLLNPF 165  
QY 181 FPGSGNIHY---NEKFGKATLTADK-SSSTAYMQLSLT----FEDSAVYFC 225  
DB 166 YPKDINVMKIDGSEBRQNGVLNSWTDQDSKDSYMSSTLTLTLDKDYERHNSYTC 220  
RESULT 8  
Q569W9\_MOUSE PRELIMINARY; PRT; 468 AA.

AC Q569W9; 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN Name=Igh-1a;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RX MDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC092271; AAH92271.1; -, mRNA.  
DR SNR: Q569W9; 20-464.  
DR MGI: MGI:96443; Igh-1a.  
DR GO: 0003823; F-antigen binding; IEA.  
DR InterPro: IPR003599; IG.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG-cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR003596; IG\_v.  
DR Pfam: PF07654; Cl-sect; 3.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IGcl; 3.  
DR SMART: SM00406; IGv; 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;  
Query Match 24.5%; Score 501.5; DB 2; Length 468;  
Best Local Similarity 53.0%; Pred. No. 3e-29;  
Matches 105; Conservative 21; Mismatches 53; Indels 19; Gaps 3;  
QY 123 GGGGSEVOLLEQSGAEIVRPGTSVKISCKASGYAFNTYMLGWKORPGHGLEWIGDI 182  
DB 14 TAGVHSEVO-LOQSGAEIVRPGTSVKISCKASGYAFNTYMLGWKORPGHGLEWIGDI 72  
QY 183 GSGNIHYNEKFGKATLTADKSSSTAYMQLSLTFFEDSAVYFCARLNLMDPMDYQCGT 242  
DB 73 GNGTTEYNEKFGKATLTADKSSSTAYMQLSLTFFEDSAVYFCARLNLMDPMDYQCGT 132  
QY 243 TVTVSSGGGSDIKLQOQSGAEIARP-----GASVMSCKTSGYTFRTYTMWVKOR 293

Db 133 TITVSSA-----KTAASVYPLAPVCGDTTSSVTLGCLVKGVPPEPTLTLMNSGS 183  
Qy 294 PGOGLEWIGYINPSRGYT 311  
Db 184 LSSGVHTPPAVLQSDLT 201

RESULT 9

HV02\_MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sime J., Rabbits T.H., Estees P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
RT immunoglobulin heavy chain."  
RL Science 216:309-311(1982).  
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL: J00493; AAA8128.1; -, mRNA.  
CC  
CC HSP; P01747; 140.  
DR HSP; P01746; 20-140.  
DR InterPro: IPR007110; Ig-1like.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 Ig heavy chain V region 93G7.  
FT DOMAIN 20 139 Ig-1like.  
FT NON\_TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CB8B31DASCE8 CRC64;  
Query Match 24.4%; Score 500; DB 1; Length 140;  
Best Local Similarity 74.8%; Pred. No. 8.9e-30;  
Matches 95; Conservative 9; Mismatches 21; Indels 2; Gaps 1;  
Qy 248 SGGGSGDILQSGAEIARPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINPS 307  
Db 14 TAGVSHVQLQSGAEIARPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINPS 73  
Qy 308 RGYTNQKFKKATLTITDKSSSTAYMQLSLTSEDSAVYYCAR--YYDHYCLDYWGQG 365  
Db 74 NGIYNNEKFKGKTLITLVKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYFDYWGQG 133  
Qy 366 TLTIVSS 372  
Db 134 TPLTVSS 140  
RESULT 10  
HV03\_MOUSE STANDARD; PRT; 120 AA.  
AC P01747;

DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Ig heavy chain V region 36-65.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83131846; PubMed=6186498;  
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,  
RA Marshak-Rothstein A.;  
RT "The genetic basis of antibody production: the dominant anti-arsenate  
RT idiotype response of the strain A mouse."  
RL Eur. J. Immunol. 12:1023-1032(1982).  
[2]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.  
RX MEDLINE=21529949; PubMed=11673524;  
RA Parhaml-Seren B., Viswanathan M., Strong R.K., Margolies M.N.;  
RT "Structural analysis of mutants of high-affinity and low-affinity p-  
RT azophenylarsenate-specific antibodies generated by alanine scanning of  
RT heavy chain complementarity-determining region 2."  
RL J. Immunol. 167:5129-5135(2001).  
CC -1- MISCELLANEOUS: From analysis of the sizes of several other  
CC differentiated genes that hybridize to this one, the authors  
CC conclude that all of these V regions have rearranged to the same J  
CC segment, JH2.  
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR; A94264; HVMSCG7.  
DR PDB; 1JFO; X-ray; H=1-120.  
DR Ensembl; ENSMUSG0000021155; Mus musculus.  
DR InterPro: IPR007110; Ig-1like.  
DR InterPro: IPR003596; Ig\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW 3D-structure; Hybridoma; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT DOMAIN 1 111 Ig-1like.  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13307 MW; FF04EA4167B654AF CRC64;

Query Match 24.4%; Score 499; DB 1; Length 120;  
Best Local Similarity 78.3%; Pred. No. 8.7e-30;  
Matches 94; Conservative 7; Mismatches 17; Indels 2; Gaps 1;  
Qy 255 IYLOQSGAEIARPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINPSRGYTN 314  
Db 1 VOLQSGAEIARPGASVSKSCSTGYTFRTYTMHWKORPGGLEWIGYINSGNTTKN 60  
Qy 315 QKFKKATLTITDKSSSTAYMQLSLTSEDSAVYYCAR--YYDHYCLDYWGQG 372  
Db 61 EKFKGKTLITLVKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYFDYWGQDTLTIVSS 120  
RESULT 11  
HV07\_MOUSE STANDARD; PRT; 139 AA.  
AC P01751; P01752;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig heavy chain V region B1-8/186-2 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muroidae; Muridae; Murinae; Mus.  
 CC NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234546; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;  
 RA Bothwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "heavy chain variable region contribution to the NpB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";   
 RL Cell 24:625-637(1981).  
 CC -1- MISCELANEOUS: The Bl-8 mu chain mRNA was cloned from a hybridoma  
 CC making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl  
 CC (NpB antibodies).  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL, J00529, AAA38170.1, -, mRNA.  
 DR PIR, A90809, MHMS18.  
 DR PDB, 1A6U; X-ray; H=20-139.  
 DR PDB, 1A6V; X-ray; H/I/J=20-139.  
 DR PDB, 1A6W; X-ray; H=20-139.  
 DR PDB, 1NGP; X-ray; H=20-139.  
 DR PDB, 1NGQ; X-ray; H=20-139.  
 DR PDB, 1NOB; X-ray; A/C=20-139.  
 DR Ensemble; ENSMUSG0000063737; Mus musculus.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT CHAIN 1  
 FT REGION 20 139 Ig heavy chain V region Bl-8/186-2.  
 FT REGION 20 49 Framework-1.  
 FT REGION 50 54 Complementarity-determining-1.  
 FT REGION 55 68 Framework-2.  
 FT REGION 69 85 Complementarity-determining-2.  
 FT REGION 86 117 Framework-3.  
 FT REGION 118 124 D segment.  
 FT REGION 125 139 JH2 segment.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 139 139  
 FT STRAND 22 24  
 FT STRAND 28 31  
 FT TURIN 33 34  
 FT STRAND 37 44  
 FT HELIX 48 50  
 FT STRAND 52 58  
 FT TURIN 60 61  
 FT STRAND 64 70  
 FT TURIN 72 74  
 FT STRAND 77 79  
 FT HELIX 81 83  
 FT TURIN 84 86  
 FT STRAND 87 92  
 FT TURIN 93 96  
 FT STRAND 97 102  
 FT HELIX 107 109  
 FT STRAND 111 118  
 FT TURIN 120 123  
 FT STRAND 129 129  
 FT STRAND 133 137  
 SO SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 23.9%; Score 489.5; DB 1; Length 139;  
 Best Local Similarity 72.0%; Pred. No. 5.4e-29;  
 Matches 95; Conservative 12; Mismatches 20; Indels 5; Gaps 2;

QY 244 VTVSGGGSGSDIKLQSGAEIAPGASVXNSCTSGYTFRTYTMHWKORPGGLEWIGY 303  
 Db 10 LAATAGVHSQVQLQPGALVYPGASVKRLSCASGYTFTSYMMHWKQRPGRGLEWIGR 69  
 QY 304 INPSRGYTNQKPFKDKATITTTKSSSTAMQSLTSSESAVYYCCARYDDHY---CLD 360  
 Db 70 IDNSGGTKXNEKFKKATLTVDKPSSTAYMQLSSLTSEDSAVYYCCARY--DYGGSSYFD 127  
 QY 361 YMGQGTTLTVSS 372  
 Db 128 YMGQGTTLTVSS 139  
 RESULT 12  
 Q4V9V8\_MOUSE PRELIMINARY; PRT; 590 AA.  
 AC Q4V9V8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=Igh-6;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muroidae; Muridae; Murinae; Mus.  
 CC NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loughlin N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huijk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC096667; AA956667.1, -, mRNA.  
 DR MGI; MGI:96448; Igh-6.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SO SEQUENCE 590 AA; 64892 MW; D42518F9A180B14 CRC64;

Query Match 23.9%; Score 489; DB 2; Length 590;

	Best Local Similarity	75.6%	Pred. No.	3.5e-28	Matches	96	Conservative	11	Mismatches	16	Indels	4	Gaps	2
Qy	122	PGSGGGGSEVQLLEDSGAELVRPRTSVKISCKASGYAFNWLGMVKORPGHGLEWIGDIF	181											
Db	13	GTAGVAVHCQVQ_LKOSGAELVRPGASVKLRCSKASYTFPDYIYNWKQRPGGLIEWIRIV	71											
Qy	182	PGSGNIHNENRFRKGATITADKSSTAYTMOLSSLTFEDSAYVFCAFLRNMDPEMDYWGOG	241											
Db	72	PGSGNTYYNEKRFGKATLTAEKSSSTAYMOLSLTSEDSAVYFCART--GTGMDYWGGG	128											
Qy	242	TFTVTYS 248												
Db	129	TSVTYS 135												
RESULT 13														
ID	Q92AR0_MOUSE	PRELIMINARY;	PRT;	143 AA.										
AC	Q92AR0;													
DT	01-DEC-2001 (TREMBLrel. 19, Created)													
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)													
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)													
DE	VH186.2-D-J-C mu protein (Fragment).													
GN	Name=VH186.2-D-J-C mu;													
OS	Mus musculus (Mouse).													
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;													
CC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;													
OX	Muridae; Murinae; Mus.													
RN	NCBI_TaxID=10090;													
RP	[1]													
RA	NUCLEOTIDE SEQUENCE.													
RC	STRAIN=C57BL/6;													
RD	Kozono Y., Kozono H., Azuma T.;													
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.													
RN	[2]													
RP	NUCLEOTIDE SEQUENCE.													
RA	Published=135311;													
RX	Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;													
RT	"Allogeneic manipulation of the GAP idiotypic cascade. Immunization of													
RT	C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-													
RT	specific V genes as the original antigen.";													
RL	J. Immunol. 141:779-784(1988).													
RL	(3)													
RN	NUCLEOTIDE SEQUENCE.													
RP	PubMed=2499887;													
RA	Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;													
RT	"Two murine natural polyreactive autoantibodies are encoded by													
RT	nonmutated germ-line genes.";													
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).													
DR	EMBL; AB067790; BAB63275.1; -; mRNA.													
DR	PIR; F28833; F28833.													
DR	PIR; F32932; F32932.													
DR	PIR; PH1105; PH1105.													
DR	PIR; PH1108; PH1108.													
DR	PIR; PH1114; PH1114.													
DR	PIR; PH1118; PH1118.													
DR	PIR; PH1119; PH1119.													
DR	PIR; PH1125; PH1125.													
DR	PIR; PH1126; PH1126.													
DR	PIR; PH1128; PH1128.													
DR	PIR; PH1129; PH1129.													
DR	PIR; PH1131; PH1131.													
DR	PIR; PH1134; PH1134.													
DR	PIR; PH1137; PH1137.													
DR	PIR; PH1139; PH1139.													
DR	PIR; PH1142; PH1142.													
DR	PIR; PH1144; PH1144.													
DR	PIR; PH1147; PH1147.													
DR	PIR; PH1149; PH1149.													
DR	PIR; PH1150; PH1150.													
DR	PIR; PH1151; PH1151.													
DR	PIR; PH1152; PH1152.													

```

DR PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R0; 1-134.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 23.8%; Score 486.5; DB 2; Length 143;
Best Local Similarity 76.3%; Pred. No. 9.4e-29;
Matches 90; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

QY 255 IKLOQSGAEIARPGASVYMGSCGTGYFTFRTYTMHWKORPGQGLEWIGYINSPRGYTYN 314
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 VOLQDQPGELVKPASPASVYLSCKASGYFTSYTMHWKORPGRGLWIGRIDPNSGCTKYN 61

QY 315 QKFKDKATLTDDKSSFTAYMQLSSLTSEDSAVYYCARYDDHYCIDYWGQGTTLTVSS 372
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 EKFSKATLTVDKFSSTAYMQLSSLTSEDSAVYYCAR-WDDDYAMDYWGQGSITVSS 118

RESULT 14
Q924P8_MOUSE PRELIMINARY; PRT; 140 AA.
ID Q924P8_MOUSE
AC Q924P8;
DT 01-DEC-2001 (TREMBLrel. 19; Created)
DT 01-DEC-2001 (TREMBLrel. 19; Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
DE V23-D-J-C mu protein (Fragment).
DE Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Euarhontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=313311;
RA Corbet S., Hirt M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB069917; BAB63933.1; -, mRNA.
DR PIR; I28833; I28833.
DR HSSP; PH1156; PH1156.
DR HSSP; P01751; 1A6W.
DR SMR; Q924P8; 1-126.
DR WGI; WGI:3576502; AB069917.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 23.7%; Score 485; DB 2; Length 140;
Best Local Similarity 78.8%; Pred. No. 1.2e-28;
Matches 93; Conservative 6; Mismatches 15; Indels 4; Gaps 1

QY 255 IKLOSGAEIARPGASVYMGSCGTGYFTFRTYTMHWKORPGQGLEWIGYINSPRGYTYN 314
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 VOLQDQGTGLVYKPGASVYLSCKASGYFTSYTMHWKORPGQGLEWIGYINSPRGYTYN 61

```

315 OKFKDALKLTIDKSSSTAYMOLSLTSDSAVYCARYYADHDHCJDYMGQGTTLTVSS 372

Db 62 EKFKSKALITLTDKSSSTACTQLSLSITSBDSAIVYCARWMD----FDYMGQGTTLTVSS 115

RESULT 15  
Q9DBL4\_MOUSE PRELIMINARY; PRT; 473 AA.

ID Q9DBL4\_MOUSE PRELIMINARY;  
AC Q9DBL4\_2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810606009 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.  
DS Name=Igh-1a;  
OS Mus musculus (Mouse).  
OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CC NCBI\_TaxID=10090;  
CX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(19)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino H., Itoh M., Ishii Y., Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Flisckmann W., Gaasterland T., Gissi C., King B., Kochia H., Kuell P., Lewis S., Matsumoto Y., Nakado I., Pesole G., Quackenbush J., Schirini L.M., Strubbi F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G., Blakesley D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M., Guerinich S., Hill D., Hofman M., Home D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima Y., Mazzarelli U., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohzuki S., Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
[3]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Pancreas;  
RT The PANTOM Consortium,  
RA "the RIKEN Genome Exploration Research Group Phase I & II Team,"  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
[4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;

RA Shobhakar A., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Kitajima T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto S., Matsunoto H., Sakaguchi S., Iyegami T., Kasahagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Iwata M., Ohara E., Watabiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaka S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "Riken integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multichipillary sequencer." ;  
RL Genome Res. 10:1757-1771 (2000).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Atakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai T.,  
RA Sogabe Y., Suzuki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL, AK007918, BAB25349.1; -, mRNA.  
DR PIR: PH1165, PH1165.  
DR PIR: S19966, S19966.  
DR PIR: S26746, S26746.  
DR HSSP: P01864, 1BOG.  
DR SMR: Q9DBL4: 20-469.  
DR Ensembl, ENSMUSG00000054328; Mus musculus.  
DR MG1: MGI:96463; IgH-1a.  
DR GO: GO:0042571; C:immunoglobulin complex, circulating; IDA.  
DR GO: GO:0005771; C:multivesicular body; IDA.  
DR GO: GO:0003823; F:antigen binding; IDA.  
DR GO: GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.  
DR GO: GO:0003033; P:antigen processing; IDA.  
DR GO: GO:0006958; P:complement activation, classical pathway; IDA.  
DR GO: GO:0045022; P:early endosome to late endosome transport; IDA.  
DR GO: GO:0008333; P:endosome to lysosome transport; IDA.  
DR GO: GO:0006911; P:phagocytosis, engulfment; IDA.  
DR GO: GO:0006910; P:phagocytosis, recognition; IDA.  
DR GO: GO:0050871; P:positive regulation of B cell activation; IDA.  
DR GO: GO:0050766; P:positive regulation of immune response; IDA.  
DR GO: GO:0001812; P:positive regulation of phagocytosis; IDA.  
DR GO: GO:0001788; P:positive regulation of type I hypersensitivity; IDA.  
DR GO: GO:0003062; P:regulation of proteolysis and peptidolysis; IDA.  
DR InterPro: IPR007110; Ig-like.  
DR InterPro: IPR003597; Ig-cl.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF07654; C1-set; 3.  
DR SMART: SM00406; IGV: 1.  
DR PROSITE: PS50835; IG\_LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
KW Immunoglobulin domain.  
SQ SEQUENCE 473 AA; 51699 MM; 90DE57A514475FBB CRC64;  
  
Query Match 23.7%; Score 485; DB 2; Length 473;  
Best Local Similarity 50.2%; Pred. No. 5,3e-28;  
Matches 109; Conservative 20; Mismatches 56; Indels 32; Gaps 4  
  
OY 123 GGGGSEVQLLEGGAEIVRPGTSVKSISCKRSGAFTNYMLGVYQRPDGHLEWIGDIFP 182  
DB 14 TAGVHCVOV LKSGAGELVKGASVKSISCKRSGTTFIDYINMWKQRPQGLLEWIGKIGP 72  
OY 183 GSGNIHYNEKRGKATLTADKSSSTAYWQLSGLTFEDSAVYFCALRLRWDEPMDYWGOST 242  
DB 73 GSGSTYYNEKRGKATLTADKSSSTAYWQLSGLTFEDSAVYFCARSGDYDIDFAVWGOST 132  
OY 243 TTVVSSGG-----GSGDILKQSGAGELARKGASVKNKSCKSGITFTTYTMW 289

Db	133	LVTISA	AKTAP	SVYPL	APVCGI	-----	TGSSVT	UGCLVK	GIFP	BPVITL	TW	179
Qy	290	VKOR	PGGLE	WIGY	INPS	RGYTN	YNQK	FKD	KATL	ITD		326
Db	180	NSGL	SSGV	HTFP	ALOG	LYT---	LSSSV	TVTS	N			211

Search completed: March 6, 2006, 14:48:20  
Job time : 113 secs

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Qy	Db	Qy	Db
280	313	340	373
YTFTRATYMHVKKOR	YASRSMNMVWVKOR	TSEDSAVYYTAR--	TSVDSAVYFCARGNTVV
PGCGLEMI	PGQGLEMI	YTDHHCID	VPYMDWGG
IGYNPS	IGRITPGD	YMGQGT	GLTVVSS
SGYNNYQK	PDNNYNGK	RTLLVSS	407
PKDRAITL	KGRATIL		
TPDSSSTAY	TLADSSSTAY		
MOQSL	MOQSL		
339	372		

RESULT 2  
US-11-116-939-11

```

1 Sequence 11, Application US//11116939
2 Publication No. US20050265995A1
3 GENERAL INFORMATION:
4 APPLICANT: Stephen Tomlinson
5 TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
6 FILE REFERENCE: 19113.0115U2
7 CURRENT APPLICATION NUMBER: US/11/116,939
8 CURRENT FILING DATE: 2005-04-28
9 PRIOR APPLICATION NUMBER: 60/565,907
10 PRIOR FILING DATE: 2004-04-28
11 NUMBER OF SEQ ID NOS: 27
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 11
14 LENGTH: 824
15 TYPE: PR1
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
19 OTHER INFORMATION: construct
20 US-11-116-939-11

```

Query Match	48.5%	Score 992.5;	DB 7;	Length 824;
Best Local Similarity	61.8%	Pred. No. 1.4e-55;		
Matches 204; Conservative	26;	Mismatches 53;	Indels 47;	Gaps 6;

```

Oy      1 ELVWTOSSPSLTVTAGEKVTMCSKSSQSLNSGNOKNTLTYOQKRPQ9PRLTLLIYMASTR 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      25 DYMSSQSPSSLAVSYGEKTMCKSSQSL--KTNOKNITAMYOQKRPQSPRLTLLIYMASSR 82
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      61 ESGVPDRFTSSGSGTDFLLTSSVQAEDLAVYYCONDYSPLTFGAGTKLEIKGGGGSGG 120
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      83 ESGVPDRFTSSGSGTDFLLTSSVKAEIDLAVYYCOQYYSPLTFGAGTKLEIKGGGGSGG 142
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      121 GSGSGGG-----SIVQLLESGAEILVRGTSVKISCSASGATPTNY 161
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      143 GSGSGGGSSMGMSCVMLFVATATGVSQVO--LEQSGPELVRGYSVKISCKSGSGTFTFDY 201
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      162 WLGAVVQORPGHGLEWIGDIFPGSGNITHYNEKFGKATLTADSSSTAWMQSLSTFEDSA 221
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      202 AIHHVVKSHAKSLJEMIGIVISTYYGHHYNOQKPKGRKRLTVLDSSSTYATMELARLTSEBSA 261
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      222 VYFCARLRNWD-----PMDYWGQGTTVTVSSGGGGSDIKLQSGAEILAP----- 267
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      262 IYVCARPNNNYSSPRPYAMDQMGQSTVTVSSGGGGSGGGSGGSCPAPLFPYAKPI 321
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy      268 -----GASVYKMSCKTSGTFTFRITM 287
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      322 NPDTDSFTPVGTSLKTECR--PGYIKQOFISI 350
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 3  
US-11-116-939-12  
Sequence 12, Application US/11116939  
Publication No. US20050265995A1  
GENERAL INFORMATION:  
APPLICANT: Stephen Tomlinson  
APPLICANT: Richard J. Oulgg  
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS  
FILE REFERENCE: 19113.011502  
CURRENT APPLICATION NUMBER: US/11/116,939

```

: CURRENT FILING DATE: 2005-04-28
: PRIOR APPLICATION NUMBER: 60/566,907
: PRIOR FILING DATE: 2004-04-28
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 412
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
: OS-11-116-939-12

```

Query Match	48.5%	Score 992;	DB 7;	Length 412;
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Matches 203; Conservative 24; Mismatches 41; Indels 42; Gaps 6;

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QY      1 ELVMTQSPSSLLPVITGAEKVTMSCKSSQSLNLSGNQKYLITWYQOKPQPPKLLIYMASTR 60
Db      25 DIVMSGSPSSLVAVSGEKVTMCKSSQSL-KTMQKYLITWYQOKPQOSPKLLIYMASSR 82
QY      61 EGSVDPFRFGSGSGGTDFTLLITISVQAEDLAVYYCONDYSPYLPFGAGTKLEIKGGGSGG 120
Db      83 EGSVDPFRFTGSGSGGTDFTLLITISVQAEDLAVYYQYVYSPYLPFTGAGTKLEIKGGGSGG 142
QY      121 GGSGGG-----SEVQLLREQSGAEIVRPGTSVKISCKAGVAFNTY 161
Db      143 GSGGGGSGMGSCWMLFLVATATGVAHSQVQ-LEQSGPELVIRPGVSVKISCKSGGYFTFDY 201
QY      162 WLCMWYKQRFQGHLEWIGDIPFQSGNIHNEKFKGKATILTDKSSSTAYMQLSLTFEDSA 221
Db      202 AITMWYKQSHAKSLFELWIGVISTYTGHTTHNQKFKKATILTDKSSSNTIYMEIALTSEDSA 261
QY      222 VYFCALAEHWDE-----FMDYWGCGTTLTVSSGGGSGSDIKLQSGAELARPGAISVK----- 272
Db      262 IYYCAFPNNYGSSPPYAMDQWGQSTVTVSSGGG-----SGGGSGGGGSLRCYNC 314
QY      273 ----MSCKTS 278
Db      315 LDPVSSCKTN 324

```

## RESULT 4

```

US-11-116-939-10
Sequence 10, Application US/1116939
Publication No. US20050265995A1
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 60/565,907
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 293
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-10

```

```

Query Match      46.8%  Score 958.5;  DB 7;  Length 293;
Best Local Similarity 70.2%  Pred. No. 8.2e-54;
Matches 191;  Conservative 20;  Mismatches 34;  Indels 27;  Gaps 4.

QY      1 ELVNTGSPSSLITVAGRKVTMSCKSSQSLNAGNQKRYLITWYQOKPGQPPKLLIYMASTR 60
      ::::::::::: : ::::::::::: ::::::::::: ::::::::::: ::::::::::: :

```

```
Db 25 DVMGSPSSSLAVSGEKVTMNCSSQSL--KTNQKNTLAMYQKPGQSPKLLIYWASR 82
Qy 61 ESGVDRFTSGSGTDFLTLLTSSVQAEADLAVYYCONDYSEPLTFGAGTKLEIKGGGSGG 120
Db 83 ESGVDRFTSGSGTDFLTLLTSSVQAEADLAVYYCONDYSEPLTFGAGTKLEIKGGGSGG 142
Qy 121 GSGGGG-----SEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYY 161
Db 143 GSGGGGSGMWSVCMFLVATATGVHSQVQ--LEQSGPELVAPGVSVKISCKSGYTFDY 201
Qy 162 WLGVKORPGHGLEMIGDIPFGSGNIHNEKFGKATLTADKSSSTAYMQLSLTFEDSA 221
Db 202 AIHWKQSHAKSLMIGVISTYGGTHYNNQKFKGKATLTVDKSSNTAYMELARLISDSA 261
Qy 222 VYFCARLRNWD-----PMDYMGQGTITVYSS 248
Db 262 IYCARPNNVGSPPYYMDCMGQGTSTVYSS 293

RESULT 5
US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US 60/520,398
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/557,951
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 29
; LENGTH: 666
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-981-356A-29

Query Match 46.5%; Score 952; DB 6; Length 666;
Best Local Similarity 55.4%; Pred. No. 4.2e-53;
Matches 209; Conservative 36; Mismatches 86; Indels 46; Gaps 10;

Qy 1 ELVMTQSPBSLTPTVTAAGEKVTMSCKSSQSLNSGNQKNTLTYWQKPGQSPKLLIYWASR 60
Db 1 DIMMTQSPBSLAVSAGEKVTMSCKSSQSLVYSSNOKNTLAMYQKPGQSPKLLIYWASR 60
Qy 61 ESGVDRFTSGSGGDFLTLLTSSVQAEADLAVYYCONDYSEPLTFGAGTKLEIKGGGSGG 120
Db 61 ESGVDRFTSGSGGDFLTLLTSSVQAEADLAVYYC--HQYLSPTFGGTTLEIK----- 112
Qy 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYYLGMVKORPGHGLEMIGDI 180
Db 113 --RTVAAPSVFIFPPSDEQL--KSGTA-SVVC-----LNNFYPRAK-----VGMKVDN 157
Qy 181 PFGSGNIHNEKFGKATLTADKSSSTAYMQLSLT-----PEDSAVYFCARLRNWDPM 235
Db 158 ALQSGN-----SQESVTEQDSKDYSLSTLTLKADYEKHKVYAC-----EV 201
Qy 236 DVMGQGTITVYSSGSGGSDIKLQSGAEIARPGASVYKMSCKTSGYTFRTYTMHWKORP 295
Db 202 THQGLSSPYTKSPNRECEVQLQSGAEIVRPGTSVKISCKASGYAFNYYLIEWVKORP 261
Qy 296 QGLEWIGYINPSKGYNTNOKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYD 355
Db 262 QGLEWIGVNNPQSGGSNNYNEKFGKATLTADKSSSTAYMQLSLTSDSAVYFCAR--SG 319
Qy 356 HYCLDVMGQGTITVYSS 372
Db 320 GFYFDYMGQGTSTVYSS 336
```

```
RESULT 6
US-11-096-046-29
; Sequence 29, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; NAME/KEY: Unsure
; LOCATION: 220
; OTHER INFORMATION: Unknown amino acid
US-11-096-046-29

Query Match 46.1%; Score 942.5; DB 7; Length 667;
Best Local Similarity 55.3%; Pred. No. 1.7e-52;
Matches 209; Conservative 37; Mismatches 85; Indels 47; Gaps 11;

Qy 1 ELVMTQSPBSLTPTVTAAGEKVTMSCKSSQSLNSGNQKNTLTYWQKPGQSPKLLIYWASR 60
Db 1 DIMMTQSPBSLAVSAGEKVTMSCKSSQSLVYSSNOKNTLAMYQKPGQSPKLLIYWASR 60
Qy 61 ESGVDRFTSGSGGDFLTLLTSSVQAEADLAVYYCONDYSEPLTFGAGTKLEIKGGGSGG 120
Db 61 ESGVDRFTSGSGGDFLTLLTSSVQAEADLAVYYC--HQYLSPTFGGTTLEIK----- 112
Qy 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFNYYLGMVKORPGHGLEMIGDI 180
Db 113 --RTVAAPSVFIFPPSDEQL--KSGTA-SVVC-----LNNFYPRAK-----VGMKVDN 157
Qy 181 PFGSGNIHNEKFGKATLTADKSSSTAYMQLSLT-----PEDSAVYFCARLRNWDPM 235
Db 158 ALQSGN-----SQESVTEQDSKDYSLSTLTLKADYEKHKVYAC-----EV 201
Qy 236 DVMGQGTITVYSS--SGGGSDIKLQSGAEIARPGASVYKMSCKTSGYTFRTYTMHWKORP 294
Db 202 THQGLSSPYTKSPNRECEVQLQSGAEIVRPGTSVKISCKASGYAFNYYLIEWVKORP 261
Qy 295 QGLEWIGYINPSKGYNTNOKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYYCARYYD 354
Db 262 QGLEWIGVNNPQSGGSNNYNEKFGKATLTADKSSSTAYMQLSLTSDSAVYFCAR--S 319
Qy 355 DHYCLDVMGQGTITVYSS 372
Db 320 GFYFDYMGQGTSTVYSS 337
```

```
RESULT 7
US-11-084-717-21
; Sequence 21, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
```

APPLICANT: IVERSON, BRENT L.  
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES  
FILE REFERENCE: USB:723US  
CURRENT APPLICATION NUMBER: US/11/084,717  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: 60/554,324  
PRIOR FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: 10/620,278  
PRIOR FILING DATE: 2003-07-15  
PRIOR APPLICATION NUMBER: 60/396,058  
PRIOR FILING DATE: 2002-07-15  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-084-717-21

Query Match 42.1%; Score 860.5; DB 7; Length 247;  
Best Local Similarity 65.7%; Pred. No. 1e-47;  
Matches 167; Conservative 31; Mismatches 43; Indels 13; Gaps 3;

QY 1 ELVWTQSPSSLTVTAGKRYTMCKSSQSLNSGNOKNYLTWYQOKPQPPKLIYMASTR 60  
DB 1 DIQMTQTSSLSASLDKRVITISCRASODI-----RNYLWYQOKPQPPKLIYYSRL 54  
QY 61 ESGVPRFTSGSGGTDFTLTISVQAEADLVYVCONDYSYPLTFGAGTKLEIK-----G 114  
DB 55 QSGVPSRFSGSGGTDSLITSNQEDIGTYFCQGNLTLPWTFGGGTKEIKRGGGSG 114  
QY 115 GGGSGGGSGGGSEVOLLEQSGAEIVRPSTSVKISCKAGYAFNTWYLGWYQRPQGL 174  
DB 115 GGGSGGGSGGGSEVO-LQSGPELVKPGASVKISCKDGYAFSSMMWVWYQRPQGL 173  
QY 175 EWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDP 234  
DB 174 EWIGRIYPGDGTNNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARSGLLRYA 233  
QY 235 MDYWGQGTIVTVSS 248  
DB 234 MDYWGQGTIVTVSS 247

RESULT 8  
US-11-179-244-21

Sequence 21, Application US/11179244  
Publication No. US20050267294A1  
GENERAL INFORMATION:  
APPLICANT: HARVEY, BARRETT R.  
APPLICANT: GEORGIU, GEORGE  
APPLICANT: IVERSON, BRENT L.  
TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS  
FILE REFERENCE: USB:721US  
CURRENT APPLICATION NUMBER: US/11/179,244  
CURRENT FILING DATE: 2005-07-12  
PRIOR APPLICATION NUMBER: US/10/620,049  
PRIOR FILING DATE: 2003-07-15  
PRIOR APPLICATION NUMBER: 60/396,058  
PRIOR FILING DATE: 2002-07-15  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-179-244-21

Query Match 42.1%; Score 860.5; DB 7; Length 247;  
Best Local Similarity 65.7%; Pred. No. 1e-47;  
Matches 167; Conservative 31; Mismatches 43; Indels 13; Gaps 3;

QY 1 ELVWTQSPSSLTVTAGKRYTMCKSSQSLNSGNOKNYLTWYQOKPQPPKLIYMASTR 60  
DB 1 DIQMTQTSSLSASLDKRVITISCRASODI-----RNYLWYQOKPQPPKLIYYSRL 54  
QY 61 ESGVPRFTSGSGGTDFTLTISVQAEADLVYVCONDYSYPLTFGAGTKLEIK-----G 114  
DB 55 QSGVPSRFSGSGGTDSLITSNQEDIGTYFCQGNLTLPWTFGGGTKEIKRGGGSG 114  
QY 115 GGGSGGGSGGGSEVOLLEQSGAEIVRPSTSVKISCKAGYAFNTWYLGWYQRPQGL 174  
DB 115 GGGSGGGSGGGSEVO-LQSGPELVKPGASVKISCKDGYAFSSMMWVWYQRPQGL 173  
QY 175 EWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDP 234  
DB 174 EWIGRIYPGDGTNNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARSGLLRYA 233  
QY 235 MDYWGQGTIVTVSS 248  
DB 234 MDYWGQGTIVTVSS 247

RESULT 9  
US-11-084-055B-21

Sequence 21, Application US/11084055B  
Publication No. US2006002947A1  
GENERAL INFORMATION:  
APPLICANT: GEORGIU, GEORGE  
APPLICANT: JEONG, KI JUN  
APPLICANT: IVERSON, BRENT L.  
TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY  
FILE REFERENCE: USB:722US  
CURRENT APPLICATION NUMBER: US/11/084,055B  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: 60/554,260  
PRIOR FILING DATE: 2004-03-18  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 247  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-084-055B-21

Query Match 42.1%; Score 860.5; DB 7; Length 247;  
Best Local Similarity 65.7%; Pred. No. 1e-47;  
Matches 167; Conservative 31; Mismatches 43; Indels 13; Gaps 3;

QY 1 ELVWTQSPSSLTVTAGKRYTMCKSSQSLNSGNOKNYLTWYQOKPQPPKLIYMASTR 60  
DB 1 DIQMTQTSSLSASLDKRVITISCRASODI-----RNYLWYQOKPQPPKLIYYSRL 54  
QY 61 ESGVPRFTSGSGGTDFTLTISVQAEADLVYVCONDYSYPLTFGAGTKLEIK-----G 114  
DB 55 QSGVPSRFSGSGGTDSLITSNQEDIGTYFCQGNLTLPWTFGGGTKEIKRGGGSG 114  
QY 115 GGGSGGGSGGGSEVOLLEQSGAEIVRPSTSVKISCKAGYAFNTWYLGWYQRPQGL 174  
DB 115 GGGSGGGSGGGSEVO-LQSGPELVKPGASVKISCKDGYAFSSMMWVWYQRPQGL 173  
QY 175 EWIGDIFPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDP 234  
DB 174 EWIGRIYPGDGTNNYNGKFKGKATLTADKSSSTAYMQLSLTSDSAVYFCARSGLLRYA 233  
QY 235 MDYWGQGTIVTVSS 248

Db 234 MDYWGQGSTVTSS 247

RESULT 10  
US-11-084-717-23

```

Sequence 23 Application US/11084717
Publication No. US20050260736A1
GENERAL INFORMATION:
APPLICANT: GEORGIOU, GEORGE
APPLICANT: JEONG, KI-JUN
APPLICANT: HARVEY, BARRETT R.
APPLICANT: IYERSON, BRENT L.
TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
FILE REFERENCE: US78:723US
CURRENT APPLICATION NUMBER: US/11/084,717
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,224
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 10/620,278
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,058
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-084-717-23

```

Query Match	40.6%;	Score 830.5;	DB 7;	Length 247;
Best Local Similarity	63.4%;	Pred. No. 7.7e-46;		
Matches 161;	Conservative 33;	Mismatches 47;	Indels 13;	Gaps 3

QY	1	ELVWMOQSPSLVTVTAGEKXTMCKSQSLNSGNQNYLTWYQOKGQOPKLIYASTR	60
QY	1	DIOMTQTISSLSASLADRVTSCKRASQDI-----RNYLWYQOKKDDGYTKFLITYTSRL	54
QY	61	ESGVDRFTGSGSGTDFLTITSSVQADLAVVYQNDYSPYLTFGAGTKLEIK-----G	114
DB	55	QGVSVSRFSGSGSGTFTYSLTINLLEQEDIGITYFCQOQNPMPFMFGGCTKLEIRGGGSD	114
QY	115	GGSGSGGGGGGGSEYQULEQSSAEILVRGTSYKISCKASGVAFTWYMLGWYKORPEHGL	174
DB	115	GGSGSGGGGGGGGSEVQ-LQOSSPELVTKPAASKISCKSGVAFNSNMWVYQORPEQGL	173
QY	175	EMIGDIFPSSGNIHYNEKEFKRKATLTADKSSSTAYNQSLSTPEDSAVYFCARLRWDEP	234
DB	174	EMIGRIYPCDDGDSNNGKFEKGKAITLADKSSSTAYNQSLSTVDSAVYFCARSGLLRYA	233
QY	235	MDYWGQGTITYVSS	248
DB	234	MDYWGQGTIVTVSS	247

RESULT 11  
US-11-179-244-23  
; Sequence 23, Application US/11179244  
; Publication No. US20050267294A1

/ APPLICANT: HARVEY, BARRETT R.  
 / APPLICANT: GEORGIOU, GEORGE  
 / APPLICANT: IVERSON, BRENT L.  
 / TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS  
 / FILE REFERENCE: UTSB:721US  
 / CURRENT APPLICATION NUMBER: US/1/179,244  
 / CURRENT FILING DATE: 2005-07-12  
 / PRIOR APPLICATION NUMBER: US/10/620,049  
 / PRIOR FILING DATE: 2003-07-15  
 /

```

; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1

```

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; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-179-244-23

```

[illegible]

```

RESULT 12
US-11-084-055B-23
/ Sequence 23, Application US/11084055B
/ Publication No. US20060029947A1
/ GENERAL INFORMATION:
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: JEONG, KI JUN
/ APPLICANT: IYERSON, BRENT L.
/ TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
/ FILE REFERENCE: UTSB:72205
/ CURRENT APPLICATION NUMBER: US/11/084,055B
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: 60/554,260
/ PRIOR FILING DATE: 2004-03-18
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-084-055B-23

```

Query Match	40.6%;	Score 830.5;	DB 7;	Length 247;
Best Local Similarity	63.4%;	Pred. No. 7.7e-46;		
Matches 161;	Conservative 33;	Mismatches 47;	Indels 13;	Gaps 3

```
QY      1 ELVMTQSPBLSLVITAGEKRTYMSCKSSQSILNSGNQKNVLTWQQKGQPPKLLIYASTR   60
        ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 DIQMQTTSLSASLSDRPRTVSCRASQDI-----RNINLWVQKKDGYTKFLIYTSTR    54
QY      61 ESGVPDRFTGSGSGCTFLLTISVAEDLAIVYYCQNDYSPLTFAGATKLEIK-----G   114
```

Db 55 QPQVPERFSGGSGGTYSLTINNLEQEDIGTYPCQQGNTPMTFGGKLTLEIKRGGGSD 114

Qy 115 GGGSGGGSGGGSEVOLLKSGAELVVRPOTSXYKISCKASGYAFNTVMYLGWTKRPGHGL 174

Db 115 GGGSGGGSGGGSEVO-LQOQSPBELVYKPPASXYKISCKQSGYAFNFMNMYKQRPQGL 173

Qy 175 EMIGDIPFGSGNTHYNEKFKGKATLTADKSSSTAYMQLSLTLPEDSAVYFCARLRNWDPE 234

Db 174 EMIGRIYFGGDSNYNEKFKGKALTLADKSSSTAYMQLSLTISVDSAVYFCARSLGLRYA 233

Qy 235 MDYWGQGTIVTVSS 248

Db 234 MDYWGQGTIVTVSS 247

```

RESULT 13
US-11-084-717-25
; Sequence 25, Application US/11084717
; Publication No. US20050260736A1
; GENERAL INFORMATION:
; APPLICANT: GEORGIOU, GEORGE
; APPLICANT: JEONG, KI-JUN
; APPLICANT: HARVEY, BARRETT R.
; APPLICANT: IYERSON, BRENT L.
; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
; FILE REFERENCE: USB:723US
; CURRENT APPLICATION NUMBER: US/11/084,717
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/554,324
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 10/620,278
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,058
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-084-717-25

```

	Query Match	Similarity	40.3%	Score 825.5	DB 7	Length 247
	Best Local	Similarity	63.4%	Pred. No. 1,66-45		
	Matches	161	Conservative	32	Mismatches 46	Indels 13
						Gaps 3
QY	1	ELVNTQSPSLTVTAGEKVTMSCKSSGSLNSGNOKNTLTYQKPGPPKLLIYMASTR	60			
Db	1	DIOMTQTTSSLSASAGDRVTVSCRSASOI-----RNLINMYOOKPDDTVFLIYYSRL	54			
QY	61	ESGVPDRFTSGSGGDTFLTISVVAEDLAVYYCONDYSYLPFGAGKLEIK-----G	114			
Db	55	LPQVPSRRSGSGSGTDSLITNNLEQEDIGITYFQQGNTVPTPTPGGKIKLEIKGGGSSD	114			
QY	115	GGGSGGGGSGGGGSEVQLLEQSGAEIYVPGTISVKISCAASGYAFLNYYLGMVKQRPFGGL	174			
Db	115	GGGSGGGGSGGGGSEVO--LQSGPELVKPGASVKISCDSGAFAFSSMNNWYKQRPQGL	173			
QY	175	EMIGIDIPGSGNIIHNEKFKATLTAAKSSSTAYMQLSLTFFEDSAVYFCARLNNMDEP	234			
Db	174	EMIRGIYQGDSDSNNGKFEKAILITADKSSSTAYMQLSLTSSVDSAVYFCARSLALYA	233			
QY	235	MDYMGQGTIVYSS 248				
Db	234	MDYMGQGTIVYSS 247				

RESULT 14  
US-11-179-244-25

```

? Sequence 25: Application US/11/179244
? Publication No. US20050267294A1
? GENERAL INFORMATION:
? APPLICANT: HARVEY, BARRETT R.
? APPLICANT: GEORGIOU, GEORGE
? APPLICANT: IVERSON, BRENT L.
? TITLE OF INVENTION: ANTIBODIES WITH INCREASED AFFINITIES FOR ANTHRAX ANTIGENS
? FILE REFERENCE: US8-721US
? CURRENT APPLICATION NUMBER: US/11/179,244
? CURRENT FILING DATE: 2005-07-12
? PRIOR APPLICATION NUMBER: US/10/620,049
? PRIOR FILING DATE: 2003-07-15
? PRIOR APPLICATION NUMBER: 60/396,058
? PRIOR FILING DATE: 2002-07-15
? NUMBER OF SEQ. ID NOS: 25
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 25
? LENGTH: 247
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? US-11-179-244-25

```

	Query Match	Best Local Match	Similarity	40.3%	Score	825.5	DB 7	Length	247
	Matches	161	Conservative	63.4%	Pred.	No. 1.66-45	Mismatches	48	Indels
								13	Gaps
									3
Qy	1	ELVWTGSSSLITTAGKRYTMCKSSQSLNSGNOKATLTYOQKPGQPKLLIYMASTR	60						
Db	1	DIQMTQTTSLSASALGRVTYVSCRASODI-----RNLNMYOQKPGDVTVFLLIYSRL	54						
Qy	61	ESGVPRFTFGSGSGSTDEFTLLTSSVOABDLAVYYCOMDYSYELTFGAGTKLEIK-----G	114						
Db	55	LPGPVPSRFSFGSGSGSTDYSLTINLNLEQEDIGTFYCGQGNTPPMTFGCGTKLEIKRGGGSD	114						
Qy	115	GGSGGGGGSGGGSGEVQLLEBSGAEIYRPRGTSVVISCSAGSYAFNMYLGMWYORPGHGL	174						
Db	115	GGSGGGGGSGGGSGEVQ-LQSGGELVAPGASVKISCDSGIAFNSSPMANWYKQKPPGGL	173						
Qy	175	EWIIDIPFGSGINHYNEKFKGATLTADKSSSTAYMQLSLLTFBDAVYFCARLNNMDEP	234						
Db	174	EWIGRIYPGDDSDSYNKGFEKGALITLADKSSSTAYMQLSITSVDASVAYFCARSGLLRYA	233						
Qy	235	MDYWGQGTYYTVSS	248						
Db	234	MDYWGQGTSTVSS	247						

```

RESULT 15
US-11-084-055B-25
Sequence 25, Application US/11084055B
Publication No. US2006002947A1
GENERAL INFORMATION:
APPLICANT: GEORGIOU, GEORGE
APPLICANT: JESONG, KI JUN
APPLICANT: IYERSON, BRENT L.
TITLE OF INVENTION: COMBINATORIAL PROTEIN LIBRARY SCREENING BY
TITLE OF INVENTION: PERIPLASMIC EXPRESSION
FILE REFERENCE: UTSB:722US
CURRENT APPLICATION NUMBER: US/11/084,055B
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: 60/554,260
PRIOR FILING DATE: 2004-03-18
NUMBER OF SEQ. ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 247
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

OTHER INFORMATION: Peptide  
US-11-084-055B-25

Query Match 40.3%; Score 825.5; DB 7; Length 247;  
Best Local Similarity 63.4%; Pred. No. 1.6e-45;  
Matches 161; Conservative 32; Mismatches 48; Indels 13; Gaps 3;

```

Qy      1 ELVMTOSPPSLVTYAGEKVTWCKSSQSLNSGNQKNYLTWYQOKPGQPPKLLIYMASTR 60
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 DIQMTQTSSLSASLGDRVTVSCRASQDI-----RNYLNMWYQOKPDGTVKFLIYTSRL 54
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      61 ESGVPDRFTGSGGTDFTLTISVQAEPLAVYICQNDYSYPLTRGAGTKLEIK-----G 114
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      55 LPGVPSRFRSGSGGTDYSLITINNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGGGSD 114
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      115 GGGSGGGSGGGSGGVOLLBOGAEIVRPGTSVKISCKASGYAFTNMYLGMVKORPGHGL 174
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      115 GGGSGGGSGGGSGGEVQ-LQSGPELVKPGASVKISCKDSGYAFNISMNMVKORPGQGL 173
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      175 EMIGDIPFGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDEP 234
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      174 EMIGRIYFGDDSNYNGKFEKGKILTTADKSSSTAYMQLSLTSVDSAVYFCARSGILRYA 233
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy      235 MDYMGQGTFTTVSS 248
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      234 MDYMGQGTSTTVSS 247
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```

Search completed: March 6, 2006, 13:22:29  
Job time : 35 secs

**This Page Blank (usptc)**

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 13:19:02 ; Search time 80 Seconds  
(without alignments)  
1974.244 Million cell updates/sec

Title: US-10-743-697-1

Perfect score: 2046  
Sequence: 1 ELVMTQSPSSLTFTAGEKVT.....LDYWGQGTTLTVSSHHHHH 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_Main:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pdp:\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pdp:\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pdp:\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pdp:\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pdp:\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pdp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	100.0	378	5	US-10-743-697-1
2	1484.5	72.6	495	3	US-09-948-004-18
3	1484.5	72.6	495	5	US-10-672-932-18
4	1467	71.7	500	4	US-10-168-809-22
5	1439.5	70.4	499	5	US-10-805-177-111
6	1414	69.1	492	4	US-10-682-845-59
7	1409	68.9	492	4	US-10-682-845-87
8	1407	68.8	492	4	US-10-682-845-65
9	1406	68.7	492	4	US-10-682-845-67
10	1406	68.7	492	4	US-10-682-845-63
11	1405	68.7	492	4	US-10-682-845-71
12	1405	68.7	492	4	US-10-682-845-69
13	1404	68.6	492	4	US-10-682-845-73
14	1401	68.5	492	4	US-10-682-845-85
15	1401	68.5	492	4	US-10-682-845-85
16	1399	68.4	492	4	US-10-682-845-77
17	1397	68.3	492	4	US-10-682-845-75
18	1397	68.3	492	4	US-10-682-845-83
19	1395	68.2	492	4	US-10-682-845-79
20	1390	67.6	492	4	US-10-682-845-81
21	1326.5	64.8	524	5	US-10-805-177-113
22	1305	63.8	532	6	US-11-036-098-18
23	1289	63.0	507	4	US-10-239-656-47
24	1189.5	58.1	895	4	US-10-296-085A-17
25	1189.5	58.1	895	4	US-10-296-085A-27
26	1189.5	58.1	895	5	US-10-496-179-4
27	1189.5	58.1	896	4	US-10-296-085A-17

28	1189.5	58.1	896	4	US-10-296-085A-26	Sequence 26, Appl
29	1189.5	58.1	896	5	US-10-496-179-2	Sequence 2, Appl
30	1189.5	58.1	895	5	US-10-496-179-7	Sequence 7, Appl
31	1189.5	58.1	899	4	US-10-296-085A-28	Sequence 28, Appl
32	1189.5	58.1	899	5	US-10-496-179-5	Sequence 5, Appl
33	1186.5	58.0	895	4	US-10-296-085A-20	Sequence 20, Appl
34	1186.5	58.0	896	4	US-10-296-085A-18	Sequence 18, Appl
35	1186.5	58.0	896	5	US-10-496-179-3	Sequence 3, Appl
36	1186.5	55.6	510	4	US-10-239-656-49	Sequence 49, Appl
37	1185.5	55.5	510	4	US-10-239-656-79	Sequence 79, Appl
38	1181.5	55.3	505	4	US-10-239-656-75	Sequence 75, Appl
39	1128.5	55.2	503	4	US-10-239-656-73	Sequence 73, Appl
40	1124.5	55.0	499	4	US-10-239-656-77	Sequence 77, Appl
41	1087	53.1	503	4	US-10-239-656-77	Sequence 350, App
42	1070.5	52.3	768	4	US-10-207-655-350	Sequence 115, App
43	1070.5	52.3	768	5	US-10-627-556-115	Sequence 11, Appl
44	955	46.7	456	4	US-10-634-862-11	Sequence 221, App
45	954	46.6	562	5	US-10-987-454-221	

ALIGNMENTS

RESULT 1					
US-10-743-697-1					
Sequence 1, Application US/10743697					
Publicatation No. US20050136050A1					
GENERAL INFORMATION:					
APPLICANT: KUFER, PETER					
APPLICANT: BERRY, MERRY					
APPLICANT: BAUELER, PATRICK					
APPLICANT: ITIN, CHRISTIAN					
TITLE OF INVENTION: BISPECTIFIC ANTIBODIES					
FILE REFERENCE: DEBB:02805					
CURRENT APPLICATION NUMBER: US/10/743,697					
CURRENT FILING DATE: 2003-12-22					
NUMBER OF SEQ ID NOS: 1					
SOFTWARE: Patent Ver. 2.1					
SEQ ID NO 1					
LENGTH: 378					
TYPE: PRT					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Description of Artificial Sequence: Synthetic					
US-10-743-697-1					
Query Match					
Best Local Similarity 100.0%; Score 2046; DB 5; Length 378;					
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ELVMTQSPSSLTFTAGEKVTMSCKSSQSLNSGNQNTVYQKPGQPPKLLIYASTR	60		
DB	1	ELVMTQSPSSLTFTAGEKVTMSCKSSQSLNSGNQNTVYQKPGQPPKLLIYASTR	60		
QY	61	EGGVDRFTGSSGSDFTLTSSVQAEDLAIVYVYCONDSYPLFGAGTLEIKGGGSGG	120		
DB	61	EGGVDRFTGSSGSDFTLTSSVQAEDLAIVYVYCONDSYPLFGAGTLEIKGGGSGG	120		
QY	121	GGSGGGSGSVQLLESGAEIVRPGTSVKISKASGAFNTYMLGWKORPGHLEWIGDI	180		
DB	121	GGSGGGSGSVQLLESGAEIVRPGTSVKISKASGAFNTYMLGWKORPGHLEWIGDI	180		
QY	181	FGSGNIHNEKFKGATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMYWGQ	240		
DB	181	FGSGNIHNEKFKGATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMYWGQ	240		
QY	241	GTTVYSSGGGSDITKLOSGAEIARPGASVMSCKTSYTFRTYTMHWKORPGGLEW	300		
DB	241	GTTVYSSGGGSDITKLOSGAEIARPGASVMSCKTSYTFRTYTMHWKORPGGLEW	300		
QY	301	IGYINSPRYTNNQFKDKATLTDDKSSSTAYMQLSLTFEDSAVYCARYYDDHYCID	360		

Db 301 IGYINPBGYNTNNQKFKDRAKTLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360  
Qy 361 YMGQGTTLTVSSHHHHH 378  
Db 361 YMGQGTTLTVSSHHHHH 378

RESULT 2  
US-09-948-004-18  
; Sequence 18, Application US/09948004  
; Publication No. US20030017979A1  
; GENERAL INFORMATION:  
; APPLICANT: MACK, Matchias  
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in  
; TITLE OF INVENTION: Immunological disorders  
; FILE REFERENCE: E 2411 EP  
; CURRENT APPLICATION NUMBER: US/09/948,004  
; CURRENT FILING DATE: 2001-09-05  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-948-004-18

Query Match 72.6%; Score 1484.5; DB 3; Length 495;  
Best Local Similarity 74.7%; Pred. No. 4.2e-91;  
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;

Qy 1 ELVMTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVLTGSPASLSASVGETVTITCRASENIV-----SYLAWYQKQKSPQLLVYNAKTL 54  
Qy 61 ESGVPRFTGSGSGTDTLTITSSVQAEPLAVYCONDYSPYLTFGAGTKLEIKGGGSGG 120  
Db 55 TBGVPSRFGSGSGGTQSLKINSLOPEDFGNYFCOHNYDTPRTFGGQTKLEIKGGGSGG 114  
Qy 121 GSGGSGGSEVQLLEQSGAEIVRPGTSYKISCKASGAFYTNWLGWVKORPGHLEWIGDI 180  
Db 115 GSGGSGGSGVQ-LQOPGAGRVPRGASVYKLSCKASGYSTSTYMMWVVKORPGGLEWIGMI 173  
Qy 181 FPGSGNIHYNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYPCARLRNWDPEMDYWGQ 240  
Db 174 HPSDSETRLNQKFNDRATLTVDKYSTAYIQLSSPTSEDSAVYYCAGEYYGIFDYWGQ 233  
Qy 241 GTTVYSSGGGSGSDIKLQOSGAEIARPGASVYKSGTSGYTFRTYTMHWVKORPGGLEW 300  
Db 234 GTTVYSSGGGSGSDIKLQOSGAEIARPGASVYKSGTSGYTFRTYTMHWVKORPGGLEW 293  
Qy 301 IGYINPBGYNTNNQKFKDRAKTLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360  
Db 294 IGYINPBGYNTNNQKFKDRAKTLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 353  
Qy 361 YMGQGTTLTVSS 372  
Db 354 YMRQGTTLTVSS 365

RESULT 3  
US-10-672-932-18  
; Sequence 18, Application US/10672932  
; Publication No. US20050191702A1  
; GENERAL INFORMATION:  
; APPLICANT: MACK, Matchias  
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in  
; TITLE OF INVENTION: Immunological disorders  
; FILE REFERENCE: E 2411 EP  
; CURRENT APPLICATION NUMBER: US/10/672,932  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: US/09/948,004  
; PRIOR FILING DATE: 2001-09-05  
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-672-932-18

Query Match 72.6%; Score 1484.5; DB 5; Length 495;  
Best Local Similarity 74.7%; Pred. No. 4.2e-91;  
Matches 278; Conservative 34; Mismatches 53; Indels 7; Gaps 2;

Qy 1 ELVMTGSPSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLWYQKPGQPPKLLIYMASTR 60  
Db 1 DIVLTGSPASLSASVGETVTITCRASENIV-----SYLAWYQKQKSPQLLVYNAKTL 54  
Qy 61 ESGVPRFTGSGSGTDTLTITSSVQAEPLAVYCONDYSPYLTFGAGTKLEIKGGGSGG 120  
Db 55 TBGVPSRFGSGSGGTQSLKINSLOPEDFGNYFCOHNYDTPRTFGGQTKLEIKGGGSGG 114  
Qy 121 GSGGSGGSEVQLLEQSGAEIVRPGTSYKISCKASGAFYTNWLGWVKORPGHLEWIGDI 180  
Db 115 GSGGSGGSGVQ-LQOPGAGRVPRGASVYKLSCKASGYSTSTYMMWVVKORPGGLEWIGMI 173  
Qy 181 FPGSGNIHYNEKFKKATLTADKSSSTAYMQLSLTFEDSAVYPCARLRNWDPEMDYWGQ 240  
Db 174 HPSDSETRLNQKFNDRATLTVDKYSTAYIQLSSPTSEDSAVYYCAGEYYGIFDYWGQ 233  
Qy 241 GTTVYSSGGGSGSDIKLQOSGAEIARPGASVYKSGTSGYTFRTYTMHWVKORPGGLEW 300  
Db 234 GTTVYSSGGGSGSDIKLQOSGAEIARPGASVYKSGTSGYTFRTYTMHWVKORPGGLEW 293  
Qy 301 IGYINPBGYNTNNQKFKDRAKTLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 360  
Db 294 IGYINPBGYNTNNQKFKDRAKTLTTDKSSSTAYMQLSLTSEDSAVYYCARYYDDHYCLD 353  
Qy 361 YMGQGTTLTVSS 372  
Db 354 YMRQGTTLTVSS 365

RESULT 4  
US-10-168-809-22  
; Sequence 22, Application US/10168809  
; Publication No. US20030180799A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller-Hermelink, Hans Konrad  
; APPLICANT: GREINER, AXEL  
; APPLICANT: DORKEN, BERND  
; APPLICANT: BARGOU, RALF  
; APPLICANT: KUPER, PETER  
; TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS  
; FILE REFERENCE: 009848-0272298  
; CURRENT APPLICATION NUMBER: US/10/168,809  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: PCT/EP00/13238  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: DE 199 62 583.2  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no  
; OTHER INFORMATION: natural origin  
US-10-168-809-22

Query Match 71.7%; Score 1467; DB 4; Length 500;  
Best Local Similarity 76.4%; Pred. No. 6.2e-90;  
Matches 285; Conservative 29; Mismatches 55; Indels 4; Gaps 4;

```

Qy 1 ELVMTGSSSLTATAGKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMASTR 60
Db 1 DIVMTQPLTLSTVIGQPASLSCKSSQSLNDS-DGKTYLNLQRPQSPRLISTLVSKL 59
Qy 61 ESGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIK-GGGGSG 119
Db 60 DSGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIKGGGSG 119
Qy 120 GGGSGGSGSEVQLEQSGAEFLVRPGTSVKISCKASGAFNTYMLGWKORPGHLEWIGD 179
Db 120 GGGSGGSGSQVQ-LQSGSEPLVKTGASVKISCKSGSYFSGVYMHVWQSHKREWIGY 178
Qy 180 IFPGSGNHINEKRGKATLTADKSSSTAYVQSLTSEDSAVYFCARLRNMDPMDYWG 239
Db 179 ISGVNPDRTYNNQKRGKATFTVIDISSRTAYVQFNSLTSEDSAVYFCAR-GGYGYVDYWG 237
Qy 240 QGTTVTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKORPGGLE 299
Db 238 QGTTVTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKORPGGLE 297
Qy 300 WIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDDHYCL 359
Db 298 WIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDDHYCL 357
Qy 360 DYWGQGTTLTVSS 372
Db 358 DYWGQGTTLTVSS 370

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RESULT 5

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US-10-805-177-111
; Sequence 111, Application US/10805177
; Publication No. US20050084449a1
GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Tse, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Meeri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABCUR 006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-111

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Query Match 70.4%; Score 1439.5; DB 5; Length 499;
Best Local Similarity 71.4%; Pred. No. 4,2e-88;
Matches 270; Conservative 41; Mismatches 58; Indels 9; Gaps 3;
Qy 1 ELVMTGSSSLTATAGKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMASTR 60
Db 1 DIVMTQPLTLSTVIGQPASLSCKSSQSLNDS-DGKTYLNLQRPQSPRLISTLVSKL 59
Qy 61 ESGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIKGGGSGG 120
Db 61 ASGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIKGGGSGG 120
Qy 121 GGGSGGSGSEVQLEQSGAEFLVRPGTSVKISCKASGAFNTYMLGWKORPGHLEWIGD 180
Db 121 GGGSGGSGSQVQ-LQSGSEPLVKTGASVKISCKSGSYFSGVYMHVWQSHKREWIGY 178

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Db 121 GGGSGGSGSQVQLEQSGAEFLVRPGTSVKISCKASGAFNTYMLGWKORPGHLEWIGD 179
Qy 181 IFPGSGNHINEKRGKATLTADKSSSTAYVQSLTSEDSAVYFCARLRNMDPMDYWG 239
Db 180 WYDSNKLTVADSVGRFTLRDMSKNTLYQMSLRADPDAVYFCADYDYNDSRHMG- 237
Qy 235 MDYWGQGTTLTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKOR 294
Db 238 FDTYWGQGTTLTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKOR 297
Qy 295 GQGLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDD 354
Db 298 GQGLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDD 357
Qy 355 DHYCLDYWGQGTTLTVSS 372
Db 358 DHYCLDYWGQGTTLTVSS 375

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RESULT 6

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US-10-682-845-59
; Sequence 59, Application US/10682845
; Publication No. US20040162411A1
GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682, 845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv EpcAMxCD3 (modified antiCD3 VH-region derived from OKT-3)
US-10-682-845-59

```

```

Query Match 69.1%; Score 1414; DB 4; Length 492;
Best Local Similarity 71.2%; Pred. No. 2.1e-86;
Matches 265; Conservative 43; Mismatches 54; Indels 10; Gaps 4;
Qy 1 ELVMTGSSSLTATAGKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKLLIYMASTR 60
Db 1 DIQLTQSKFMSTSVGDVSVYTKRASQ-----NVGTNAVYQKPGQSPKALISASVYR 54
Qy 61 ESGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIKGGGSGG 120
Db 55 YSGVDFPTSGSGTDFTLTITSSVQAEFLAVYCONDSYPLTFGAGTKLEIKGGGSGG 114
Qy 121 GGGSGGSGSEVQLEQSGAEFLVRPGTSVKISCKASGAFNTYMLGWKORPGHLEWIGD 180
Db 115 GGGSGGSGSQVQ-LQSGSEPLVKTGASVKISCKSGSYFSGVYMHVWQSHKREWIGY 173
Qy 181 IFPGSGNHINEKRGKATLTADKSSSTAYVQSLTSEDSAVYFCARLRNMDPMDYWG 240
Db 174 WSG-GSTDYNAAFIRLRLISKDMSKQVFFKMSIQADNTALYYCARHENS--FAYWQ 230
Qy 241 GTTVTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKORPGGLEW 300
Db 231 GTTVTVSSGGGSDIKLQSGAEFLARPGASVKMSCKTSGYTFRTYTMHVWVQKORPGGLEW 290
Qy 301 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDDHYCLD 360
Db 291 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYVQSLTSEDSAVYFCARYDDHYCLD 350
Qy 361 YWGQGTTLTVSS 372
Db 351 YWGQGTTLTVSS 375

```

Db 351 YMGQGTTLTVSS 362

RESULT 7

US-10-682-845-61

/ Sequence 61, Application US/10682845

/ Publication No. US20040162411A1

/ GENERAL INFORMATION:

/ APPLICANT: Lanzavecchia, Antonio

/ TITLE OF INVENTION: Potent T cell modulating molecules

/ FILE REFERENCE: G2296 US

/ CURRENT APPLICATION NUMBER: US/10/682,845

/ CURRENT FILING DATE: 2003-10-10

/ PRIOR APPLICATION NUMBER: US 60/419,149

/ PRIOR FILING DATE: 2002-10-18

/ PRIOR APPLICATION NUMBER: CA 2,403,313

/ PRIOR FILING DATE: 2002-10-11

/ NUMBER OF SEQ ID NOS: 89

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 61

/ LENGTH: 492

/ TYPE: PRT

/ ORGANISM: artificial sequence

/ FEATURE:

/ OTHER INFORMATION: scfv EPCAMxCD3 with M1 mutant in anti-CD3 part

US-10-682-845-61

Query Match 68.9%; Score 1409; DB 4; Length 492;

Best Local Similarity 71.0%; Pred. No. 4,6e-86;

Matches 264; Conservative 44; Mismatches 54; Indels 10; Gaps 4;

Qy 1 ELVWTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60

Db 1 DIQLTQSKFMSTSVGDRSVYTCASQ-----NVGNVAMVYQKPGQSPKALITYSASR 54

Qy 61 ESGVPRFTSGSGGTDFTLTITSSVQAEADLAVVYCONDYSPPLTFGAGTKLEIKGGGSGG 120

Db 55 YSGVPRFTSGSGGTDFTLTITSSVQAEADLAVVYCONDYSPPLTFGAGTKLEIKGGGSGG 114

Qy 121 GSGGGGSEVQILEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 180

Db 115 GSGGGGSEVQILEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 173

Qy 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 240

Db 174 MSG-GSTDYNAATFSRISIKDNKSKQVFFKMSLQANDTAITYCARMENMS--FAYMGQ 230

Qy 241 GTTVTVSSGGGSDIKILOQSGAEIARPGASVKNKSGTSGYTFTRYTMHWYKORPGGLEW 300

Db 231 GTTVTVSSGGGSDIKILOQSGAEIARPGASVKNKSGTSGYTFTRYTMHWYKORPGGLEW 290

Qy 301 IGYINPRGYTNVQKFKDKATLTDDKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 360

Db 291 IGYINPRGYTNVQKFKDKATLTDDKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 350

Qy 361 YMGQGTTLTVSS 372

Db 351 YMGQGTTLTVSS 362

RESULT 8

US-10-682-845-87

/ Sequence 87, Application US/10682845

/ Publication No. US20040162411A1

/ GENERAL INFORMATION:

/ APPLICANT: Lanzavecchia, Antonio

/ TITLE OF INVENTION: Potent T cell modulating molecules

/ FILE REFERENCE: G2296 US

/ CURRENT APPLICATION NUMBER: US/10/682,845

/ CURRENT FILING DATE: 2003-10-10

/ PRIOR APPLICATION NUMBER: US 60/419,149

/ PRIOR FILING DATE: 2002-10-18

/ PRIOR APPLICATION NUMBER: CA 2,403,313

/ PRIOR FILING DATE: 2002-10-11

/ NUMBER OF SEQ ID NOS: 89

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 87

/ LENGTH: 492

/ TYPE: PRT

/ ORGANISM: artificial sequence

/ FEATURE:

/ OTHER INFORMATION: scfv EPCAMxCD3 with M76 mutant in anti-CD3 part

US-10-682-845-87

Query Match 68.8%; Score 1407; DB 4; Length 492;

Best Local Similarity 71.0%; Pred. No. 6,2e-86;

Matches 264; Conservative 44; Mismatches 54; Indels 10; Gaps 4;

Qy 1 ELVWTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60

Db 1 DIQLTQSKFMSTSVGDRSVYTCASQ-----NVGNVAMVYQKPGQSPKALITYSASR 54

Qy 61 ESGVPRFTSGSGGTDFTLTITSSVQAEADLAVVYCONDYSPPLTFGAGTKLEIKGGGSGG 120

Db 55 YSGVPRFTSGSGGTDFTLTITSSVQAEADLAVVYCONDYSPPLTFGAGTKLEIKGGGSGG 114

Qy 121 GSGGGGSEVQILEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 180

Db 115 GSGGGGSEVQILEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 173

Qy 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 240

Db 174 MSG-GSTDYNAATFSRISIKDNKSKQVFFKMSLQANDTAITYCARMENMS--FAYMGQ 230

Qy 241 GTTVTVSSGGGSDIKILOQSGAEIARPGASVKNKSGTSGYTFTRYTMHWYKORPGGLEW 300

Db 231 GTTVTVSSGGGSDIKILOQSGAEIARPGASVKNKSGTSGYTFTRYTMHWYKORPGGLEW 290

Qy 301 IGYINPRGYTNVQKFKDKATLTDDKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 360

Db 291 IGYINPRGYTNVQKFKDKATLTDDKSSSTAYVMOJSLTFEDSAVYFCARLRNMBPMDYMGQ 350

Qy 361 YMGQGTTLTVSS 372

Db 351 YMGQGTTLTVSS 362

# RESULT 9

US-10-682-845-65

/ Sequence 65, Application US/10682845

/ Publication No. US20040162411A1

/ GENERAL INFORMATION:

/ APPLICANT: Lanzavecchia, Antonio

/ TITLE OF INVENTION: Potent T cell modulating molecules

/ FILE REFERENCE: G2296 US

/ CURRENT APPLICATION NUMBER: US/10/682,845

/ CURRENT FILING DATE: 2003-10-10

/ PRIOR APPLICATION NUMBER: US 60/419,149

/ PRIOR FILING DATE: 2002-10-18

/ PRIOR APPLICATION NUMBER: CA 2,403,313

/ PRIOR FILING DATE: 2002-10-11

/ NUMBER OF SEQ ID NOS: 89

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 65

/ LENGTH: 492

/ TYPE: PRT

/ ORGANISM: artificial sequence

/ FEATURE:

/ OTHER INFORMATION: scfv EPCAMxCD3 with M7 mutant in anti-CD3 part

US-10-682-845-65

Query Match 68.7%; Score 1406; DB 4; Length 492;

Best Local Similarity 71.0%; Pred. No. 7,2e-86;

Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

Qy 1 ELVWTGSSSLTVTAGEKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60

```

Db      1 DIQLTOSQKFMSTSVGDRVSVTCRKSQ-----NVGTVNAVWYQKPGQSPKALIYSASR 54
Qy      61 ESGVDPFTGSGSGTDFLTLTISVQAEPLAVYCONDPYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPFTGSGSGTDFLTLTISVQSEDLAVYFCQONNSYPLTFGAGTKLEIKGGGSGG 114
Qy      121 GSGGGGSEVQLLBQSGAEIVRPSTSVKISCKASGYAFNNWMLGWKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGVLVQPSQSLSTCTVSGFSLTSYGVMWRQSPGKGLEWLGVI 173
Qy      181 PFGSGNIHNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISKDNKSQYFFKNSIQANDTAIYCARMENMS--PAYWGQ 230
Qy      241 GTTAVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 300
Db      231 GTTVVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 290
Qy      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 350
Qy      361 YWGQGTTLTVSS 372
Db      351 YWGQGTTLTVSS 362

```

RESULT 10

```

; Sequence 67, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M9 mutant in anti-CD3 part
US-10-682-845-67

```

Query Match 68.7%; Score 1406; DB 4; Length 492;

Best Local Similarity 71.0%; Pred. No. 7.2e-86;

Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

Qy      1 ELVMTQSPSSLTAVTAGEKYTWMSCKSQSLNSGNQKNYLTWYQKRPQGPPLKIYMASTR 60
Db      1 DIQLTOSQKFMSTSVGDRVSVTCRKSQ-----NVGTVNAVWYQKPGQSPKALIYSASR 54
Qy      61 ESGVDPFTGSGSGTDFLTLTISVQAEPLAVYCONDPYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPFTGSGSGTDFLTLTISVQSEDLAVYFCQONNSYPLTFGAGTKLEIKGGGSGG 114
Qy      121 GSGGGGSEVQLLBQSGAEIVRPSTSVKISCKASGYAFNNWMLGWKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGVLVQPSQSLSTCTVSGFSLTSYGVMWRQSPGKGLEWLGVI 173
Qy      181 PFGSGNIHNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISKDNKSQYFFKNSIQANDTAIYCARMENMS--PAYWGQ 230
Qy      241 GTTAVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 300

```

```

Db      231 GTTVVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 290
Qy      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 350
Qy      361 YWGQGTTLTVSS 372
Db      351 YWGQGTTLTVSS 362

```

RESULT 11

```

; Sequence 63, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpcAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63

```

Query Match 68.7%; Score 1405; DB 4; Length 492;

Best Local Similarity 71.0%; Pred. No. 8.4e-86;

Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

Qy      1 ELVMTQSPSSLTAVTAGEKYTWMSCKSQSLNSGNQKNYLTWYQKRPQGPPLKIYMASTR 60
Db      1 DIQLTOSQKFMSTSVGDRVSVTCRKSQ-----NVGTVNAVWYQKPGQSPKALIYSASR 54
Qy      61 ESGVDPFTGSGSGTDFLTLTISVQAEPLAVYCONDPYPLTFGAGTKLEIKGGGSGG 120
Db      55 YSGVDPFTGSGSGTDFLTLTISVQSEDLAVYFCQONNSYPLTFGAGTKLEIKGGGSGG 114
Qy      121 GSGGGGSEVQLLBQSGAEIVRPSTSVKISCKASGYAFNNWMLGWKORPGHLEWIGDI 180
Db      115 GSGGGGSGQVK-LQESGPGVLVQPSQSLSTCTVSGFSLTSYGVMWRQSPGKGLEWLGVI 173
Qy      181 PFGSGNIHNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240
Db      174 WSG-GSTDYNAFISRLSISKDNKSQYFFKNSIQANDTAIYCARMENMS--PAYWGQ 230
Qy      241 GTTAVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 300
Db      231 GTTVVSSGGGSDIKLQSGAEILARPGASVMSCKTSGYTFTRYTMHVKORPGQGLEW 290
Qy      301 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 360
Db      291 IGYINPSRGYTNYNQKFKDKATLTDDKSSSTAYMQLSLTSEDSAVYCCARYDDHYCLD 350
Qy      361 YWGQGTTLTVSS 372
Db      351 YWGQGTTLTVSS 362

```

RESULT 12

```

; Sequence 71, Application US/10682845
; Publication No. US20040162411A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EPCAMxCD3 with M1 mutant in anti-CD3 part
US-10-682-845-71

```

```

Query Match      68.7%; Score 1405; DB 4; Length 492;
Best Local Similarity 70.7%; Pred. No. 8.4e-86;
Matches 263; Conservative 45; Mismatches 54; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRSVTCKASQ-----NVGTNVAMYQKPGQSPKALITYSASR 54

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 114

QY 121 GSGGGGSEVQLLEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 GSGGGGSGQVK-LQESGPGIYVQPSQSLITCTVSGPSTISYGVHWYKQSPKGLIEMIGVI 173

QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNMDPMDYWGQ 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 MSG-GSTDYNAAFISRLSISKNSKQVFFKMSLQANDTAIYICARMEHNS--FAVWQ 230

QY 241 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKSGTGYTFRTYTMHWYKORPGGLEW 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKSGTGYTFRTYTMHWYKORPGGLEW 290

QY 301 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 350

QY 361 YMGQGTTLTVSS 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 351 YMGQGTTLTVSS 362

```

```

RESULT 13
US-10-682-845-69
; Sequence 69, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence

```

```

; FEATURE:
; OTHER INFORMATION: scfv EPCAMxCD3 with M10 mutant in anti-CD3 part
US-10-682-845-69

```

```

Query Match      68.6%; Score 1404; DB 4; Length 492;
Best Local Similarity 71.0%; Pred. No. 9.8e-86;
Matches 264; Conservative 43; Mismatches 55; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRSVTCKASQ-----NVGTNVAMYQKPGQSPKALITYSASR 54

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 114

QY 121 GSGGGGSEVQLLEQSGAEIYRPGTSVKISCKASGAFNTYMWLGWYKORPGHLEWIGDI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 115 GSGGGGSGQVK-LQESGPGIYVQPSQSLITCTVSGPSTISYGVHWYKQSPKGLIEMIGVI 173

QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNMDPMDYWGQ 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 MSG-GSTDYNAAFISRLSISKNSKQVFFKMSLQANDTAIYICARMEHNS--FAVWQ 230

QY 241 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKSGTGYTFRTYTMHWYKORPGGLEW 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 GTTIVTSSGGGSDIKLQSGAEIARPGASVKNKSGTGYTFRTYTMHWYKORPGGLEW 290

QY 301 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 IGYINPGRGTNNYQKFKDKATLTDDKSSSTAYWQLSLTSEDSAVYVCARYDDHYCLD 350

QY 361 YMGQGTTLTVSS 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 351 YMGQGTTLTVSS 362

```

```

RESULT 14
US-10-682-845-73
; Sequence 73, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: scfv EPCAMxCD3 with M13 mutant in anti-CD3 part
US-10-682-845-73

```

```

Query Match      68.5%; Score 1401; DB 4; Length 492;
Best Local Similarity 70.7%; Pred. No. 1.6e-85;
Matches 263; Conservative 44; Mismatches 55; Indels 10; Gaps 4;

```

```

QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPGQPPKLLIYMASTR 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIQLTQSKFMSTSVGDRSVTCKASQ-----NVGTNVAMYQKPGQSPKALITYSASR 54

QY 61 ESGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 55 YSGVPDRFTGSGGTDFTLTITSSVQAE DLAVVYQNDYSYPLTFGAGTKLEIKGGGSGG 114

```



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:12 ; Search time 89 Seconds  
(without alignment)  
1866.126 Million cell updates/sec

Title: US-10-743-697-1  
Perfect score: 2046  
Sequence: 1 ELVMTQSPSSITVTAGEKVT.....LDYWGCGTTLTVSSHHHHH 378

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	100.0	378	9	AEA36900 Anti-CD3x
2	1998	97.7	521	9	ADV66121 Anti-CD3-
3	1935	94.6	521	9	ADV66116 Anti-CD3-
4	1930	94.3	496	9	AD283653 CD3 speci
5	1930	94.3	496	9	AD283657 CD3 speci
6	1930	94.3	496	9	AD283645 CD3 speci
7	1892	92.5	496	9	AD283615 CD3 speci
8	1892	92.5	496	9	AD283629 CD3 speci
9	1892	92.5	515	9	AD283441 Deimmuniz
10	1859	90.9	496	9	AD283641 CD3 speci
11	1859	90.9	496	9	AD283649 CD3 speci
12	1859	90.9	496	9	AD283657 CD3 speci
13	1829	89.4	515	9	AD283436 Deimmuniz
14	1821	89.0	496	9	AD283619 CD3 speci
15	1821	89.0	496	9	AD283625 CD3 speci
16	1821	89.0	496	9	AD283633 CD3 speci
17	1821	89.0	496	9	AD283613 CD3 speci
18	1677	82.0	496	9	ADV21533 Mature fo
19	1625	79.4	506	9	AD283427 Deimmuniz
20	1623	78.9	494	9	ADV21531 Mature fo
21	1614.5	78.9	526	9	ADV6107 Anti-CD3-
22	1613.5	78.9	501	9	ADV21529 Mature fo
23	1611.5	78.8	495	9	ADV21527 Mature fo
24	1609.5	78.7	526	9	ADV66119 Anti-CD3-

25	1581	77.3	498	9	AD283582 Non-deimm
26	1581	77.3	504	9	ADV14556 Bioprecifi
27	1581	77.3	504	9	Aea52447 Human CD3
28	1581	77.3	531	3	Aay43749 Amino aci
29	1562	76.3	504	9	ADV21535 Mature fo
30	1548.5	75.7	502	9	ADV14530 Bioprecifi
31	1513	73.9	498	9	AD283574 Vector PE
32	1513	73.9	498	9	AD283578 Vector PE
33	1513	73.9	498	9	AD283576 Vector PE
34	1508.5	73.7	520	9	AD283433 Deimmuniz
35	1503.5	73.5	520	9	AD283439 Murine CC
36	1484.5	72.6	495	5	AAE22193 Vector PE
37	1475	72.1	498	9	AD283572 Vector PE
38	1475	72.1	498	9	AD283568 Vector PE
39	1475	72.1	498	9	AD283570 Vector PE
40	1470	71.8	498	9	AD283558 Vector PE
41	1470	71.8	498	9	AD283556 Vector PE
42	1470	71.8	498	9	AD283560 Vector PE
43	1466	71.7	498	9	AD283564 Vector PE
44	1466	71.7	498	9	AD283566 Vector PE
45	1466	71.7	498	9	AD283562 Vector PE

ALIGNMENTS

RESULT 1  
AEA36900  
ID AEA36900 standard; protein; 378 AA.  
XX  
AC AEA36900;  
DT 25-AUG-2005 (first entry)  
XX  
DE Anti-CD3xanti-EpCAM bispecific chimeric antibody.  
XX  
KW chimeric antibody; cytostatic; antimicrobial; antiallergic;  
KW antiinflammatory; virucide; antiparasitic; immunomodulatory;  
KW immunosuppressive; vaccine; bispecific antibody; cancer; inflammation;  
KW immune disorder; infection; viral infection; allergy;  
KW parasitic infection; graft versus host disease.  
XX  
OS Synthetic.  
XX  
PN US2005136050-A1.  
XX  
PD 23-JUN-2005.  
XX  
PF 22-DEC-2003; 2003US-00743697.  
XX  
PR 22-DEC-2003; 2003US-00743697.  
XX  
PA (KUPF/) KUPFER P.  
PA (BAEU/) BAUERLE P.  
PA (ITIN/) ITIN C.  
PI Kufer P, Berry M, Baeuerle P, Itin C;  
XX  
DR WPI; 2005-444079/45.  
XX  
PT New bispecific antibody comprising two antibody variable domains on a  
PT single polypeptide chain, useful in preparing a composition for treating  
PT or preventing proliferative, infectious or graft-versus-  
PT host disease.  
XX  
PS Claim 24; SEQ ID NO 1; 12pp; English.  
XX  
CC The invention relates to a bispecific antibody comprising two antibody  
CC variable domains on a single polypeptide chain, where a first portion of  
CC the bispecific antibody is capable of recruiting the activity of a human  
CC immune effector cell by specifically binding to an effector antigen  
CC located on the human immune effector cell, the first portion consisting

CC of one antibody variable domain; and a second portion of the bispecific  
 CC antibody is capable of specifically binding to a target antigen other  
 CC than the effector antigen, the target antigen being located on a target  
 CC cell other than the human immune effector cell, and the second portion  
 CC comprising an antibody variable domain. The bispecific antibody is useful  
 CC in preparing a composition for treating, preventing or ameliorating a  
 CC proliferative disease, a tumorous disease, an inflammatory disease, an  
 CC immunological disorder, an autoimmune disease, an infectious disease, a  
 CC viral disease, an allergic reaction, a parasitic reaction, a graft-versus  
 CC -host disease or a host-versus-graft disease. This sequence corresponds  
 CC to the chimeric anti-CD3xanti-EpCAM bispecific antibody of the invention.  
 CC  
 XX

Sequence 378 AA;

Query Match 100.0%; Score 2046; DB 9; Length 378;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-119;  
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLTWYQKPGQPKLLIYMSTR 60  
 DB 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLTWYQKPGQPKLLIYMSTR 60  
 QY 61 ESGVPDRFTSGSGSDTFTLTSSVQAEDLAVYYCONDYSPFLFGAGTKLEIKGGGSGG 120  
 DB 61 ESGVPDRFTSGSGSDTFTLTSSVQAEDLAVYYCONDYSPFLFGAGTKLEIKGGGSGG 120  
 QY 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYAFITNYMLGWVKORPGHGLEWIGDI 180  
 DB 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYAFITNYMLGWVKORPGHGLEWIGDI 180  
 QY 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRMDDEMDYWGQ 240  
 DB 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRMDDEMDYWGQ 240  
 QY 241 GTTYYVSSGGGSDIKLQSGAEIARPGASVMSCKTSGTFTFRYTHMWVKORPGGLEW 300  
 DB 241 GTTYYVSSGGGSDIKLQSGAEIARPGASVMSCKTSGTFTFRYTHMWVKORPGGLEW 300  
 QY 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTSEDSAVYYCARYYDDHYCLD 360  
 DB 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTSEDSAVYYCARYYDDHYCLD 360  
 QY 361 YMGQGTTLTVSSSHHHHHH 378  
 DB 361 YMGQGTTLTVSSSHHHHHH 378

RESULT 2

ADV66121 ID ADV66121 standard; protein; 521 AA.

ADV66121;

24-FEB-2005 (first entry)

Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 44.

bispecific single chain antibody; epithelial cell adhesion molecule;  
 EpCAM; CD3; tumor; cancer; cytosclastic.

Unidentified.

WO2004106383-A1.

09-DEC-2004.

26-MAY-2004; 2004WO-EP005687.

31-MAY-2003; 2003EP-00012133.

31-MAY-2003; 2003EP-00012134.

(MICR-) MICROMET AG.

XX

PI Kufner P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;  
 PI Kohleisen B, Lenkner-Schuetz U, Baerle P;  
 XX  
 DR WPI; 2005-021271/02.  
 DR N-PSDB; ADV66120.  
 XX  
 PT New pharmaceutical composition having a bispecific single chain antibody  
 PT construct, useful for preventing, treating or ameliorating a tumorous  
 PT disease, such as an epithelial or minimal residual cancer.  
 PS Claim 12; SEQ ID NO 44; 227bp; English.  
 XX

The invention comprises a composition that contains a bispecific single  
 CC chain antibody consisting of at least two domains, where one of domains  
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the  
 CC second domain binds to human CD3 antigen. The bispecific antibody  
 CC construct of the invention is useful for the prevention, treatment or  
 CC amelioration of a tumorous disease, such as an epithelial or minimal  
 CC residual cancer. The present amino acid sequence represents a bispecific  
 CC single chain antibody of the invention.

Sequence 521 AA;

Query Match 97.7%; Score 1998; DB 9; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-116;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLTWYQKPGQPKLLIYMSTR 60  
 DB 20 ELVMTQSPSSSLTVTAGEKVTMSCKSSQSLNSGNQKNTLTWYQKPGQPKLLIYMSTR 79  
 QY 61 ESGVPDRFTSGSGSDTFTLTSSVQAEDLAVYYCONDYSPFLFGAGTKLEIKGGGSGG 120  
 DB 80 ESGVPDRFTSGSGSDTFTLTSSVQAEDLAVYYCONDYSPFLFGAGTKLEIKGGGSGG 139  
 QY 121 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYAFITNYMLGWVKORPGHGLEWIGDI 180  
 DB 140 GSGGGGSEVQLLQSGAEIYRPQTSYKISCKASGYAFITNYMLGWVKORPGHGLEWIGDI 199  
 QY 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRMDDEMDYWGQ 240  
 DB 200 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRMDDEMDYWGQ 259  
 QY 241 GTTYYVSSGGGSDIKLQSGAEIARPGASVMSCKTSGTFTFRYTHMWVKORPGGLEW 300  
 DB 260 GTTYYVSSGGGSDIKLQSGAEIARPGASVMSCKTSGTFTFRYTHMWVKORPGGLEW 319  
 QY 301 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTSEDSAVYYCARYYDDHYCLD 360  
 DB 320 IGYINPGRGYTNYNQKFKDRAITLTDKSSSTAYWQLSLTSEDSAVYYCARYYDDHYCLD 379  
 QY 361 YMGQGTTLTVSS 372  
 DB 380 YMGQGTTLTVSS 391

RESULT 3

ADV66116 ID ADV66116 standard; protein; 521 AA.

ADV66116;

24-FEB-2005 (first entry)

Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39.

bispecific single chain antibody; epithelial cell adhesion molecule;  
 EpCAM; CD3; tumor; cancer; cytosclastic.

Unidentified.

WO2004106383-A1.

XX

PD 09-DEC-2004.  
 XX 26-MAY-2004; 2004WO-EP005687.  
 PF 31-MAY-2003; 2003EP-00012133.  
 PR 31-MAY-2003; 2003EP-00012134.  
 XX  
 XX (MICR-) MICROMET AG.  
 XX  
 XX Kufner P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;  
 PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;  
 DR WPI; 2005-021271/02.  
 DR N-PSDB; ADV66115.  
 XX  
 PT New pharmaceutical composition having a bispecific single chain antibody  
 PT construct, useful for preventing, treating or ameliorating a tumorous  
 PT disease, such as an epithelial or minimal residual cancer.  
 XX  
 PS Claim 12; SEQ ID NO 39; 227pp; English.  
 XX  
 CC The invention comprises a composition that contains a bispecific single  
 CC chain antibody consisting of at least two domains, where one of domains  
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the  
 CC second domain binds to human CD3 antigen. The bispecific antibody  
 CC construct of the invention is useful for the prevention, treatment or  
 CC amelioration of a tumorous disease, such as an epithelial or minimal  
 CC residual cancer. The present amino acid sequence represents a bispecific  
 CC single chain antibody of the invention.  
 CC  
 XX Sequence 521 AA;  
 SQ  
 Query Match 94.6%; Score 1935; DB 9; Length 521;  
 Best Local Similarity 97.0%; Pred. No. 1.2e-112;  
 Matches 361; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 ELVMTQSPSSSLVTAVGGEKVTWMSCKSSQSLNSGNOKNTLTWYQKRGQPPKLLIYMASTR 60  
 DB 20 ELVMTQSPSSSLVSAAGEKVTWMSCKSSQSLNSGNOKNTLTWYQKRGQPPKLLIYGASTR 79  
 QY 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120  
 DB 80 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 139  
 QY 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 DB 140 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 199  
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMDYMQQ 240  
 DB 200 FPGSGNAHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMDYMQQ 259  
 QY 241 GTTAVTVSSGGGSDIKLQOQSGAEIVRPGASVMSCKTSYTRTTRTMHVVKORPGGLEW 300  
 DB 260 GTTAVTVSSGGGSDIKLQOQSGAEIVRPGASVMSCKTSYTRTTRTMHVVKORPGGLEW 319  
 QY 301 IGYTPSRGTYNNQFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCID 360  
 DB 320 IGYTPSRGTYNNQFKDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARYDDHYCID 379  
 QY 361 YWGQGTLLTVSS 372  
 DB 380 YWGQGTLLTVSS 391  
 RESULT 4  
 ADZ83653  
 ID ADZ83653 standard; protein; 496 AA.  
 XX  
 AC ADZ83653;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX

DE CD3 specific binding construct SEQ ID NO 275.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KM graft versus host disease; Cytostatic; Antiinflammatory;  
 KM Immunosuppressive; Vitruicide; Antibacterial; Anti allergic; Antiparasitic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2005040220-A1.  
 XX  
 XX 06-MAY-2005.  
 XX  
 XX 15-OCT-2004; 2004WO-EP011646.  
 XX  
 XX 16-OCT-2003; 2003EP-00023581.  
 XX  
 XX (MICR-) MICROMET AG.  
 XX  
 XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;  
 PI Carr FU, Hamilton AA, Williams S;  
 XX  
 XX WPI; 2005-333494/34.  
 DR N-PSDB; ADZ83652.  
 XX  
 XX  
 PT New cytotoxically active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 XX  
 PS Claim 20; SEQ ID NO 275; 639pp; English.  
 XX  
 CC The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.  
 XX  
 SQ Sequence 496 AA;  
 Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2.4e-112;  
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ELVMTQSPSSSLVTAVGGEKVTWMSCKSSQSLNSGNOKNTLTWYQKRGQPPKLLIYMASTR 60  
 DB 1 ELVMTQSPSSSLVTAVGGEKVTWMSCKSSQSLNSGNOKNTLTWYQKRGQPPKLLIYMASTR 60  
 QY 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120  
 DB 61 ESGVDRFTGSGSGTDFTLTITSSVQAEDLAVYYCONDYSYPLTFGAGTKLEIKGGGSGG 120  
 QY 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 DB 121 GSGGGGSEVQLLEQSGAEIVRPGTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMDYMQQ 240  
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNMDPMDYMQQ 240  
 QY 241 GTTAVTVSSGGGSDIKLQOQSGAEIVRPGASVMSCKTSYTRTTRTMHVVKORPGGLEW 300  
 DB 241 GTTAVTVSSGGGSDIKLQOQSGAEIVRPGASVMSCKTSYTRTTRTMHVVKORPGGLEW 300

QY 301 IGYINPGRGYTNNQKFKDRAITLTDKSSSTAYWQSLTSBDSAVYYCARYYDDHYCLD 360  
 DB 301 IGYINPGRGYTNNQKFKDRVITITTDKSTSTAYWELSLNSBPTAVYYCARYYDDHYCLD 360  
 QY 361 YMGQGITLVVSS 372  
 DB 361 YMGQGITLVVSS 372

## RESULT 5

AD283637  
 ID AD283637 standard; protein; 496 AA.  
 AC AD283637;  
 XX 14-JUL-2005 (first entry)  
 DT 14-JUL-2005 (first entry)  
 DE CD3 specific binding construct SEQ ID NO 259.  
 XX  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KM graft versus host disease; cytostatic; antiinflammatory;  
 KW immunosuppressive; virucide; antibacterial; antiallergic; antiparasitic.  
 XX Synthetic.  
 OS  
 PN WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX 15-OCT-2004; 2004WO-EP011646.  
 PF 15-OCT-2004; 2004WO-EP011646.  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 PA (MICR-) MICROMET AG.  
 PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX WPI: 2005-333494/34.  
 DR N-PSDB; AD283636.  
 XX  
 PT New cytotoxically active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT proliferative disease.  
 PT  
 PT Claim 20, SEQ ID NO 259; 639pp; English.

XX The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2,4e-112;  
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSLTITVAERKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKRLIYWASTR 60

DB 1 ELVMTQSPSSLTITVAERKVTMSCKSSQSLNSGNQKNTLWYQKPGQPKRLIYWASTR 60  
 QY 61 ESGVPRFSGSGSGTFTLTLSISVQAEADLAVYYCONDYSPILTFGATKLEIKGGGSGG 120  
 DB 61 ESGVPRFSGSGSGTFTLTLSISVQAEADLAVYYCONDYSPILTFGATKLEIKGGGSGG 120  
 QY 121 GSGGGGSEVQLLEQGAELVRPQTSVKISCKASGYAFITNYWIGMKORPGHLEWIGDI 180  
 DB 121 GSGGGGSEVQLLEQGAELVRPQTSVKISCKASGYAFITNYWIGMKORPGHLEWIGDI 180  
 QY 181 PFGSGNIHYNEKKGKATLTADKSSSTAYWQSLTFEDSAVYFCARLRWDEPMYWGQ 240  
 DB 181 PFGSGNIHYNEKKGKATLTADKSSSTAYWQSLTFEDSAVYFCARLRWDEPMYWGQ 240  
 QY 241 GTTVTVSSGGGSDIKLQSGAEELARPGASVKKSCKTSGYTFTRYTMHWYKORPGQLEW 300  
 DB 241 GTTVTVSSGGGSDVQLVSGAEVKKPGASVKKSCASGTFTRYTMHWYKORPGQLEW 300  
 QY 301 IGYINPGRGYTNNQKFKDRAITLTDKSSSTAYWQSLTSBDSAVYYCARYYDDHYCLD 360  
 DB 301 IGYINPGRGYTNNQKFKDRVITITTDKSTSTAYWELSLNSBPTAVYYCARYYDDHYCLD 360  
 QY 361 YMGQGITLVVSS 372  
 DB 361 YMGQGITLVVSS 372

## RESULT 6

AD283645  
 ID AD283645 standard; protein; 496 AA.  
 AC AD283645;  
 XX 14-JUL-2005 (first entry)  
 DT 14-JUL-2005 (first entry)  
 DE CD3 specific binding construct SEQ ID NO 267.  
 XX  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KM graft versus host disease; cytostatic; antiinflammatory;  
 KW immunosuppressive; virucide; antibacterial; antiallergic; antiparasitic.  
 XX Synthetic.  
 OS  
 PN WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX 15-OCT-2004; 2004WO-EP011646.  
 PF 15-OCT-2004; 2004WO-EP011646.  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 PA (MICR-) MICROMET AG.  
 PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,  
 PI Carr FJ, Hamilton AA, Williams S;  
 XX WPI: 2005-333494/34.  
 DR N-PSDB; AD283644.  
 XX

XX The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease.  
 CC  
 CC Claim 20, SEQ ID NO 267; 639pp; English.

Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2,4e-112;  
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 94.3%; Score 1930; DB 9; Length 496;  
 Best Local Similarity 95.2%; Pred. No. 2.4e-112;  
 Matches 354; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSLTITVAGEKVTWMSCKSSQSLNSGNQKYLITWYQKPGQPKLLIYMASTR 60  
 DB 1 ELVMTQSPSSLTITVAGEKVTWMSCKSSQSLNSGNQKYLITWYQKPGQPKLLIYMASTR 60  
 QY 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSYPLTGAAGTKLEIKGGGSGG 120  
 DB 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSYPLTGAAGTKLEIKGGGSGG 120  
 QY 121 GSGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 DB 121 GSGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240  
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240  
 QY 241 GTTAVTSSGGGSDIKLQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEW 300  
 DB 241 GTTAVTSSGGGSDIKLQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEW 300  
 QY 301 IGYINPSRGYTNYNQKFDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDY 360  
 DB 301 IGYINPSRGYTNYNQKFDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDY 360  
 QY 361 YWGQGTTLTVSS 372  
 DB 361 YWGQGTTLTVSS 372

RESULT 7  
 AD283615  
 ID AD283615 standard; protein; 496 AA.

XX AD283615;

DT 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 237.

XX neoplasm; inflammation; immune disorder; infection; allergy;  
 XX graft versus host disease; Cytostatic; Antiinflammatory;  
 KM immunosuppressive; Vitruicide; Antibacterial; Antiallergic; Antiparasitic.

OS Synthetic.

PN MO2005040220-AL.

PD 06-MAY-2005.

PF 15-OCT-2004; 2004MO-BE011646.

PR 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

PI Hofmeister R, Kohleisen B, Lenkkerl-Schuetz U, Itin C, Baueerle P;

PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; AD283614.

XX New cytotoxically active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.

PS Claim 20; SEQ ID NO 237; 639pp; English.

XX The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 92.5%; Score 1892; DB 9; Length 496;  
 Best Local Similarity 93.5%; Pred. No. 5.6e-110;  
 Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELVMTQSPSSLTITVAGEKVTWMSCKSSQSLNSGNQKYLITWYQKPGQPKLLIYMASTR 60  
 DB 1 ELVMTQSPSSLTITVAGEKVTWMSCKSSQSLNSGNQKYLITWYQKPGQPKLLIYMASTR 60  
 QY 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSYPLTGAAGTKLEIKGGGSGG 120  
 DB 61 ESGVPDRFTGSGSGDTFTLTISVQAEIDLAVYYCONDYSYPLTGAAGTKLEIKGGGSGG 120  
 QY 121 GSGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 DB 121 GSGSGGSEVOLLEQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEWIGDI 180  
 QY 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240  
 DB 181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDYWGQ 240  
 QY 241 GTTAVTSSGGGSDIKLQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEW 300  
 DB 241 GTTAVTSSGGGSDIKLQSGAEIVRPQTSVKISCKASGYAFITNYLGMVKORPGHGLEW 300  
 QY 301 IGYINPSRGYTNYNQKFDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDY 360  
 DB 301 IGYINPSRGYTNYNQKFDKATLTDDKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDY 360  
 QY 361 YWGQGTTLTVSS 372  
 DB 361 YWGQGTTLTVSS 372

RESULT 8  
 AD283629  
 ID AD283629 standard; protein; 496 AA.

XX AD283629;

DT 14-JUL-2005 (first entry)

DE CD3 specific binding construct SEQ ID NO 251.

```

XX      neoplasm; inflammation; immune disorder; infection; allergy;
KM      graft versus host disease; cytostatic; Antiinflammatory;
KM      Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
XX      Synthetic.
XX      WO2005040220-A1.
XX      PD
XX      06-MAY-2005.
XX      PF
XX      15-OCT-2004; 2004WO-EP011646.
XX      PR
XX      16-OCT-2003; 2003EP-00023581.
XX      PA
XX      (MICR-) MICROMET AG.
XX      PI
XX      Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,
XX      Carr FU, Hamilton AA, Williams S;
XX      WPI; 2005-333494/34.
XX      DR
XX      N-PSDB; ADZ83628.
XX      PT
XX      New cytotoxically active CD3 specific binding construct comprises a first
XX      domain specifically binding to human CD3 and an Ig-derived second binding
XX      PT domain, useful for treating, preventing, or ameliorating, e.g.
XX      PT proliferative disease.
XX      PS
XX      Claim 20; SEQ ID NO 251; 639pp; English.
XX      CC
XX      The invention relates to a cytotoxically active CD3 specific binding
XX      CC construct comprising a first domain specifically binding to human CD3 and
XX      CC an Ig-derived second binding domain. The CD3 specific binding construct
XX      CC above or the construct produced by the process, nucleic acid molecule,
XX      CC vector, or host is useful for the preparation of a pharmaceutical
XX      CC composition for the prevention, treatment, or amelioration of a
XX      CC proliferative disease, a tumor, an inflammatory disease, an immunological
XX      CC disorder, an autoimmune disease, an infectious disease, viral disease,
XX      CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
XX      CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
XX      CC construct is useful for treating, preventing, or ameliorating
XX      CC proliferative disease, a tumor, an inflammatory disease, an immunological
XX      CC disorder, an autoimmune disease, an infectious disease, viral disease,
XX      CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
XX      CC host-versus-graft diseases. The present sequence represents the amino
XX      CC acid sequence of a CD3 specific binding construct.
XX      SQ
XX      Sequence 496 AA;
XX      Query Match          92.5%; Score 1892; DB 9; Length 496;
XX      Best Local Similarity 93.5%; Pred. No. 5.6e-110;
XX      Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY      1 ELVMTQSSSLVTYAGKVTMSCKSSQSLNSGNQKXLYTVOOKPQPPKLLIYMASTR 60
DB      1 ELVMTQSSSLVTYAGKVTMSCKSSQSLNSGNQKXLYTVOOKPQPPKLLIYMASTR 60
QY      61 BSGVPDRFTSGSGGDFLTITSSVOABDLAVYVCONDSYPLFTGAGTKLEIKGGGSGG 120
DB      61 BSGVPDRFTSGSGGDFLTITSSVOABDLAVYVCONDSYPLFTGAGTKLEIKGGGSGG 120
QY      121 GSGSGGSGEVLILBOSGAEIVRPGTSVYKISCKASGYAFTNYMLGMVQKRPQGHLEWIGDI 180
DB      121 GSGSGGSGEVLILBOSGAEIVRPGTSVYKISCKASGYAFTNYMLGMVQKRPQGHLEWIGDI 180
QY      181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDWGQ 240
DB      181 FPGSGNIHYNEKFKGKATLTADKSSSTAYMQLSLTFEDSAVYFCARLRNDEPMDWGQ 240
QY      241 GTTYTSSGGGGGSDIYKLOOSGAELARPGASIVMSCKTSYGFYTYTMVMVQKRGQGLEW 300
DB      241 GTTYTSSGGGGGSDIYKLOOSGAELARPGASIVMSCKTSYGFYTYTMVMVQKRGQGLEW 300

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QY      301 IGYINPSRGYNTYNQFKOKATLTDDKSSSTAYMQLSLTFEDSAVYFCARRYDDHYCLD 360
DB      301 IGYINPSRGYNTYNADSVKGRFTITDDKSSSTAYMQLSLTFEDSAVYFCARRYDDHYCLD 360
QY      361 YMGQGTTLTYSS 372
DB      361 YMGQGTTLTYSS 372
XX      RESULT 9
XX      ID
XX      ADZ83441
XX      ADZ83441 standard; protein; 515 AA.
XX      AC
XX      ADZ83441;
XX      DT
XX      14-JUL-2005 (first entry)
XX      DE
XX      Deimmunized construct 5-10xanti-CD3.
XX      KM
XX      neoplasm; inflammation; immune disorder; infection; allergy;
XX      KM graft versus host disease; cytostatic; Antiinflammatory;
XX      KM Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
XX      OS
XX      Synthetic.
XX      PN
XX      WO2005040220-A1.
XX      PD
XX      06-MAY-2005.
XX      PF
XX      15-OCT-2004; 2004WO-EP011646.
XX      PR
XX      16-OCT-2003; 2003EP-00023581.
XX      PA
XX      (MICR-) MICROMET AG.
XX      PI
XX      Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P,
XX      Carr FU, Hamilton AA, Williams S;
XX      WPI; 2005-333494/34.
XX      DR
XX      N-PSDB; ADZ83440.
XX      PT
XX      New cytotoxically active CD3 specific binding construct comprises a first
XX      PT domain specifically binding to human CD3 and an Ig-derived second binding
XX      PT domain, useful for treating, preventing, or ameliorating, e.g.
XX      PT proliferative disease.
XX      PS
XX      Claim 20; SEQ ID NO 63; 639pp; English.
XX      CC
XX      The invention relates to a cytotoxically active CD3 specific binding
XX      CC construct comprising a first domain specifically binding to human CD3 and
XX      CC an Ig-derived second binding domain. The CD3 specific binding construct
XX      CC above or the construct produced by the process, nucleic acid molecule,
XX      CC vector, or host is useful for the preparation of a pharmaceutical
XX      CC composition for the prevention, treatment, or amelioration of a
XX      CC proliferative disease, a tumor, an inflammatory disease, an immunological
XX      CC disorder, an autoimmune disease, an infectious disease, viral disease,
XX      CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
XX      CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
XX      CC construct is useful for treating, preventing, or ameliorating
XX      CC proliferative disease, a tumor, an inflammatory disease, an immunological
XX      CC disorder, an autoimmune disease, an infectious disease, viral disease,
XX      CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
XX      CC host-versus-graft diseases. The present sequence represents the amino
XX      CC acid sequence of deimmunized construct 5-10xanti-CD3.
XX      SQ
XX      Sequence 515 AA;
XX      Query Match          92.5%; Score 1892; DB 9; Length 515;
XX      Best Local Similarity 93.5%; Pred. No. 5.8e-110;
XX      Matches 348; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY      1 ELVMTQSSSLVTYAGKVTMSCKSSQSLNSGNQKXLYTVOOKPQPPKLLIYMASTR 60

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Db 20 ELVWTOSSSLTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPCQPPKLLIYMASTR 79  
 Qy 61 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 120  
 Db 80 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 139  
 Qy 121 GSGGGGSEVQLLEQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 180  
 Db 140 GSGGGGSEVQLLEQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 199  
 Qy 181 FPGSGNIHNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240  
 Db 200 FPGSGNIHNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 259  
 Qy 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300  
 Db 260 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 319  
 Qy 301 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 360  
 Db 320 IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCLD 379  
 Qy 361 YMGQGTTLTVSS 372  
 Db 380 YMGQGTTLTVSS 391

RESULT 10  
 AD283641  
 ID AD283641 standard; protein: 496 AA.  
 XX AC AD283641;  
 DT 14-JUL-2005 (first entry)  
 DE CD3 specific binding construct SEQ ID NO 263.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antiinflammatory;  
 KW Immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.  
 XX Synthetic.  
 OS WO2005040220-A1.  
 FN 06-MAY-2005.  
 PD 15-OCT-2004; 2004WO-EP011646.  
 XX 16-OCT-2003; 2003EP-00023581.  
 PR (MICR-) MICROMET AG.  
 PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baueerle P;  
 PI Carr FJ, Hamilton MA, Williams S;  
 XX MPI; 2005-333494/34.  
 DR N-PSDB; AD283640.  
 XX New cytotoxicity active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 XX Claim 20; SEQ ID NO 263; 639pp; English.  
 XX The invention relates to a cytotoxicity active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.

XX Sequence 496 AA;

Query Match 90.9%; Score 1859; DB 9; Length 496;  
 Best Local Similarity 71.6%; Pred. No. 6,4e-108;  
 Matches 355; Conservative 11; Mismatches 6; Indels 124; Gaps 1;

Qy 1 ELVWTOSSSLTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPCQPPKLLIYMASTR 60  
 Db 1 ELVWTOSSSLTYTAGKVTMSCKSSQSLNSGNQKNYLTWYQKPCQPPKLLIYMASTR 60  
 Qy 61 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 120  
 Db 61 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 120  
 Qy 61 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 120  
 Db 61 ESVGPRFTSGSGCTDFTLTITSSVQADLAIVYCCNDYSYPLTFGAGTKLEIKGGSGG 120  
 Qy 121 GSGGGGSEVQLLEQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 180  
 Db 121 GSGGGGSEVQLLEQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 180  
 Qy 181 FPGSGNIHNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240  
 Db 181 FPGSGNIHNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNDEPMYWGQ 240  
 Qy 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300  
 Db 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300  
 Qy 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300  
 Db 241 GTTVTVSSGGGSDIKLQSGAELARPASVYKMSCKTSGYTFTRYTMHWKORPGGLEW 300  
 Qy 256  
 Db 256  
 Qy 301 YDTSKVASGVAPRPSGSGSDIDYLTINSLEADPAATYCCQMSNPITFGGKVEIKG 360  
 Db 301 YDTSKVASGVAPRPSGSGSDIDYLTINSLEADPAATYCCQMSNPITFGGKVEIKG 360  
 Qy 256  
 Db 256  
 Qy 361 EGTSTGSGSGSGGADVDVQLVQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 420  
 Db 361 EGTSTGSGSGSGGADVDVQLVQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 420  
 Qy 361 EGTSTGSGSGSGGADVDVQLVQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 420  
 Db 361 EGTSTGSGSGSGGADVDVQLVQSGAELVRPETSVKISCKASGAFYTMWLGWVQRPCHGLEWIGDI 420  
 Qy 357 YCLDYWGQGTTLTVSS 372  
 Db 481 YCLDYWGQGTTLTVSS 496

RESULT 11  
 AD283649  
 ID AD283649 standard; protein: 496 AA.  
 XX AC AD283649;  
 DT 14-JUL-2005 (first entry)  
 DE CD3 specific binding construct SEQ ID NO 271.  
 XX neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; Cytostatic; Antiinflammatory;  
 KW Immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.  
 XX Synthetic.  
 OS WO2005040220-A1.  
 FN 06-MAY-2005.  
 PD 15-OCT-2004; 2004WO-EP011646.  
 XX 16-OCT-2003; 2003EP-00023581.  
 PR (MICR-) MICROMET AG.  
 PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baueerle P;  
 PI Carr FJ, Hamilton MA, Williams S;  
 XX MPI; 2005-333494/34.  
 DR N-PSDB; AD283640.  
 XX New cytotoxicity active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 XX Claim 20; SEQ ID NO 263; 639pp; English.  
 XX The invention relates to a cytotoxicity active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological

PF 15-OCT-2004; 2004MO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 PA (MICR-) MICROMET AG.  
 XX  
 PI Hofmeister R, Kohleisen B, Lenkner-Schuetz U, Itin C, Baeuerle P,  
 PI Carr FU, Hamilton AA, Williams S;  
 XX  
 DR WPI: 2005-333494/34.  
 DR N-PSDB; AD283648.  
 PT  
 PT New cytotoxically active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 PS  
 PS Claim 20; SEQ ID NO 271; 639pp; English.  
 XX  
 CC The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.  
 XX  
 SQ Sequence 496 AA;  
 Query Match 90.9%; Score 1859; DB 9; Length 496;  
 Best Local Similarity 71.6%; Pred. No. 6.4e-108;  
 Matches 355; Conservative 11; Mismatches 6; Indels 124; Gaps 1;  
 QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKPPQPKLLIYMASTR 60  
 DB 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKPPQPKLLIYMASTR 60  
 QY 61 ESGVPDRFTGSGGSDTFTLTISVQAEPLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120  
 DB 61 ESGVPDRFTGSGGSDTFTLTISVQAEPLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120  
 QY 121 GSGGGGSEVQLLESGAGELVRPGTSYKISCKASGVAFTNWLGMVQKRGHLEWIGDI 180  
 DB 121 GSGGGGSEVQLLESGAGELVRPGTSYKISCKASGVAFTNWLGMVQKRGHLEWIGDI 180  
 QY 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDPMYWGQ 240  
 DB 181 PFGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDPMYWGQ 240  
 QY 241 GTTYTSSGGGGSDI----- 255  
 DB 241 GTTYTSSGGGGSDI----- 255  
 QY 256 ----- 255  
 DB 256 ----- 255  
 QY 301 YDTSKVASGVAPARFSGSGGTDYSLTINSLEAEDAATYYCOQMSNPITFGGCTKVEIKG 360  
 DB 301 YDTSKVASGVAPARFSGSGGTDYSLTINSLEAEDAATYYCOQMSNPITFGGCTKVEIKG 360  
 QY 256 -----KLQSGAGELARPGASVYKMSCKTGYTFRTYTMHWYKORPGQ 296  
 DB 361 EGTSTGSGGSGSGGADVDVLVQSGAEVYKXGASVYKXSCASGTYTFRYTMHWYKORPGQ 420  
 QY 297 GLEWIGIYNPBRGTYNNQKFKDKATLTDDYSSSTAYWQLSLTFEDSAVYFCARLYDDH 356  
 DB 421 GLEWIGIYNPBRGTYNNQKFKDKATLTDDYSSSTAYWQLSLTFEDSAVYFCARLYDDH 480

QY 357 YCLDYWGQGTTTLTVSS 372  
 DB 481 YCLDYWGQGTTTVSS 496  
 RESULT 12  
 ID AD283657 standard; protein; 496 AA.  
 XX  
 AC AD283657;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE CD3 specific binding construct SEQ ID NO 279.  
 XX  
 KW neoplasm; inflammation; immune disorder; infection; allergy;  
 KW graft versus host disease; cytotoxic; antineoplastic;  
 KW immunosuppressive; virucide; antibacterial; antiallergic; antiparasitic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005040220-A1.  
 XX  
 PD 06-MAY-2005.  
 XX  
 PF 15-OCT-2004; 2004MO-EP011646.  
 XX  
 PR 16-OCT-2003; 2003EP-00023581.  
 XX  
 PA (MICR-) MICROMET AG.  
 XX  
 PI Hofmeister R, Kohleisen B, Lenkner-Schuetz U, Itin C, Baeuerle P,  
 PI Carr FU, Hamilton AA, Williams S;  
 XX  
 DR WPI: 2005-333494/34.  
 DR N-PSDB; AD283656.  
 XX  
 PT New cytotoxically active CD3 specific binding construct comprises a first  
 PT domain specifically binding to human CD3 and an Ig-derived second binding  
 PT domain, useful for treating, preventing, or ameliorating, e.g.  
 PT proliferative disease.  
 PS  
 PS Claim 20; SEQ ID NO 279; 639pp; English.  
 XX  
 CC The invention relates to a cytotoxically active CD3 specific binding  
 CC construct comprising a first domain specifically binding to human CD3 and  
 CC an Ig-derived second binding domain. The CD3 specific binding construct  
 CC above or the construct produced by the process, nucleic acid molecule,  
 CC vector, or host is useful for the preparation of a pharmaceutical  
 CC composition for the prevention, treatment, or amelioration of a  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
 CC construct is useful for treating, preventing, or ameliorating  
 CC proliferative disease, a tumor, an inflammatory disease, an immunological  
 CC disorder, an autoimmune disease, an infectious disease, viral disease,  
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
 CC host-versus-graft diseases. The present sequence represents the amino  
 CC acid sequence of a CD3 specific binding construct.  
 XX  
 SQ Sequence 496 AA;  
 Query Match 90.9%; Score 1859; DB 9; Length 496;  
 Best Local Similarity 71.6%; Pred. No. 6.4e-108;  
 Matches 355; Conservative 11; Mismatches 6; Indels 124; Gaps 1;  
 QY 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKPPQPKLLIYMASTR 60  
 DB 1 ELVMTGSPSSLTVTAGKVTMSCKSSQSLNSGNQKNTLTWYQKPPQPKLLIYMASTR 60  
 QY 61 ESGVPDRFTGSGGSDTFTLTISVQAEPLAVYYCONDYSPYLTFGAGTKLEIKGGGSGG 120

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Db      |||||||
61  EGVDPRTGSGSDFTLTITSSVOAEDLAVYCONDISYPLTGAGTKLEIKGGGSGG 120
Qy      |||||||
121  GSGGGGSEVOLLBOSGAELVRPGTSVKISCKASGYAFTNYLGMVKORPGHGLEWIGDI 180
Db      |||||||
121  GSGGGGSEVOLLBOSGAELVRPGTSVKISCKASGYAFTNYLGMVKORPGHGLEWIGDI 180
Qy      |||||||
181  FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Db      |||||||
181  FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Qy      |||||||
241  GTTYVSSGGGGSDI----- 255
Db      |||||||
241  GTTYVSSGGGGSDI VLTQSPATLSLSPGERATLTCRASSSVSYMMYQQKPKAPKMI 300
Qy      |||||||
256  ----- 255
Db      |||||||
301  YDTSKVASGVAPARPSGSGSDTDYSITINSLEAEDAATYYCOQMSNPLTFGGGTKEIKG 360
Qy      |||||||
256  -----KIQSGAELARPGASVYKMSCKTSGYTFRTYTMHWVKORPGQ 296
Db      |||||||
361  EGTSTGSGSGSGGADPDVQLVQSGAEVKKPGASVKYSCKASGYFTFTYTMHWVQAPGQ 420
Qy      |||||||
297  GLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 356
Db      |||||||
421  GLEWIGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDH 480
Qy      |||||||
357  YCLDYWGQGTTLTVSS 372
Db      |||||||
481  YCLDYWGQGTTLTVSS 496

RESULT 13
AD283436
ID  AD283436 standard; protein; 515 AA.
XX
AC  AD283436;
XX
DT  14-JUL-2005 (first entry)
XX
DE  Deimmunized construct 4-1xanti-CD3.
XX
KW  neoplasm; inflammation; immune disorder; infection; allergy;
KW  graft versus host disease; Cytostatic; Antiinflammatory;
KW  immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS  Synthetic.
XX
PN  WO2005040220-A1.
XX
PD  06-MAY-2005.
XX
PF  15-OCT-2004; 2004WO-EP011646.
XX
PR  16-OCT-2003; 2003EP-00023581.
XX
PA  (MICR-) MICROMET AG.
XX
PI  Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baerlele P;
PI  Carr FU, Hamilton AA, Williams S;
XX
DR  WPI; 2005-333494/34.
XX
DR  N-PSDB; AD283435.
XX
PT  New cytotoxically active CD3 specific binding construct comprises a first
PT  domain specifically binding to human CD3 and an Ig-derived second binding
PT  domain, useful for treating, preventing, or ameliorating, e.g.
PT  proliferative disease.
XX
PS  Claim 20; SEQ ID NO 58; 639pp; English.
XX
CC  The invention relates to a cytotoxically active CD3 specific binding
CC  construct comprising a first domain specifically binding to human CD3 and

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CC  an Ig-derived second binding domain. The CD3 specific binding construct
CC  above or the construct produced by the process, nucleic acid molecule,
CC  vector, or host is useful for the preparation of a pharmaceutical
CC  composition for the prevention, treatment, or amelioration of a
CC  proliferative disease, a tumor, an inflammatory disease, an immunological
CC  disorder, an autoimmune disease, an infectious disease, viral disease,
CC  allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC  host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC  construct is useful for treating, preventing, or ameliorating
CC  proliferative disease, a tumor, an inflammatory disease, an immunological
CC  disorder, an autoimmune disease, an infectious disease, viral disease,
CC  allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC  host-versus-graft diseases. The present sequence represents the amino
CC  acid sequence of deimmunized construct 4-1xanti-CD3.
XX
SQ  Sequence 515 AA;
XX
Query Match      89.4%; Score 1829; DB 9; Length 515;
Best Local Similarity 90.6%; Pred. No. 4.9e-106;
Matches 337; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

Qy      |||||||
1  ELVMTQSPSSLTFTVAGEKVTWISCKSSQSLNSGNQKNTLTYYQKPGQPKLLIYMASTR 60
Db      |||||||
20  ELVMTQSPSSLTFTVAGEKVTWISCKSSQSLNSGNQKNTLTYYQKPGQPKLLIYMASTR 79
Qy      |||||||
61  EGVDPRTGSGSDFTLTITSSVOAEDLAVYCONDISYPLTGAGTKLEIKGGGSGG 120
Db      |||||||
61  EGVDPRTGSGSDFTLTITSSVOAEDLAVYCONDISYPLTGAGTKLEIKGGGSGG 120
Qy      |||||||
80  EGVDPRTGSGSDFTLTITSSVOAEDLAVYCONDISYPLTGAGTKLEIKGGGSGG 139
Db      |||||||
121  GSGGGGSEVOLLBOSGAELVRPGTSVKISCKASGYAFTNYLGMVKORPGHGLEWIGDI 180
Qy      |||||||
140  GSGGGGSEVOLLBOSGAELVRPGTSVKISCKASGYAFTNYLGMVKORPGHGLEWIGDI 199
Db      |||||||
181  FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 240
Qy      |||||||
200  FPGSGNIHYNEKFKGKATLTADKSSSTAYWQLSLTFEDSAVYFCARLRNWDDEPDYWGQ 259
Db      |||||||
241  GTTYVSSGGGGSDI KIQSGAELARPGASVYKMSCKTSGYTFRTYTMHWVKORPGQGLEW 300
Db      |||||||
260  GTTYVSSGGGGSDI KIQSGAELARPGASVYKMSCKTSGYTFRTYTMHWVKORPGQGLEW 319
Qy      |||||||
301  IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCID 360
Db      |||||||
320  IGYINPSRGYTNVQKFKDKATLTDDKSSSTAYWQLSLTFEDSAVYFCARLYDDHYCID 379
Qy      |||||||
361  YWGQGTTLTVSS 372
Db      |||||||
380  YWGQGTTLTVSS 391

RESULT 14
AD283619
ID  AD283619 standard; protein; 496 AA.
XX
AC  AD283619;
XX
DT  14-JUL-2005 (first entry)
XX
DE  CD3 specific binding construct SEQ ID NO 241.
XX
KW  neoplasm; inflammation; immune disorder; infection; allergy;
KW  graft versus host disease; Cytostatic; Antiinflammatory;
KW  immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS  Synthetic.
XX
PN  WO2005040220-A1.
XX
PD  06-MAY-2005.
XX
PF  15-OCT-2004; 2004WO-EP011646.
XX
PR  16-OCT-2003; 2003EP-00023581.
XX

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XX (M1CR-) MICROMET AG.  
PA Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;  
PI Carr FU, Hamilton AA, Williams S;  
XX WPI; 2005-333494/34.  
DR N-PSDB; AD283618.  
XX  
XX New cytotoxically active CD3 specific binding construct comprises a first  
PT domain specifically binding to human CD3 and an Ig-derived second binding  
PT domain, useful for treating, preventing, or ameliorating, e.g.  
PT proliferative disease.  
XX  
XX Claim 20; SEQ ID NO 241; 639pp; English.  
XX  
XX The invention relates to a cytotoxically active CD3 specific binding  
CC construct comprising a first domain specifically binding to human CD3 and  
CC an Ig-derived second binding domain. The CD3 specific binding construct  
CC above or the construct produced by the process, nucleic acid molecule,  
CC vector, or host is useful for the preparation of a pharmaceutical  
CC composition for the prevention, treatment, or amelioration of a  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
CC construct is useful for treating, preventing, or ameliorating  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The present sequence represents the amino  
CC acid sequence of a CD3 specific binding construct.  
XX  
SQ Sequence 496 AA;

Query Match 89.0%; Score 1821; DB 9; Length 496;  
Best Local Similarity 70.4%; Pred. No. 1.5e-105;  
Matches 349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;  
QY 1 ELVWTPGSSSLTVTAGKRVMSCKSSQSLNSGNQKXLYTWYQKPPQPKLLIYMASTR 60  
DB 1 ELVWTPGSSSLTVTAGKRVMSCKSSQSLNSGNQKXLYTWYQKPPQPKLLIYMASTR 60  
QY 61 ESVGPDFRTSGSGGTDFLTITSSVOAEDLAVYYCONDSYPLTFGAGTKLEIKGGGSGG 120  
DB 61 ESVGPDFRTSGSGGTDFLTITSSVOAEDLAVYYCONDSYPLTFGAGTKLEIKGGGSGG 120  
QY 121 GSGSGGSGSEVOLLEQSGAEIVRPQTSYKISCKASGYAFNTYWLGMVYKORPGHLEWIGDI 180  
DB 121 GSGSGGSGSEVOLLEQSGAEIVRPQTSYKISCKASGYAFNTYWLGMVYKORPGHLEWIGDI 180  
QY 181 PRSGNHYNKEFKGKATLTADKSSSTAYMQLSLTFPDSAVYFCARLRNWDDEMDWQ 240  
DB 181 PRSGNHYNKEFKGKATLTADKSSSTAYMQLSLTFPDSAVYFCARLRNWDDEMDWQ 240  
QY 241 GTTYSVSSGGGSDIQMTQSPSSLSASVGRVITTCRASQSVSYMNTYQKPKGAPKMTI 300  
DB 241 GTTYSVSSGGGSDIQMTQSPSSLSASVGRVITTCRASQSVSYMNTYQKPKGAPKMTI 300  
QY 256 ----- 255  
DB 301 YDTSKVASGVPARFSGSGGTGYSLTINSLBAEDATYYCOQMSNPILTFGGTKVEIKG 360  
QY 256 -----KIQSGAEIARPGASVYKSCSTGTTFRYTMHWYKORPGQ 296  
DB 361 EGTSTGSGSGSGGADVDVLVQSGAEVKKKPGASVKYSCKASGYTFRTYTHMWRQAPGQ 420  
QY 297 GLEWIGYINPARGYTNVQKFKDKATLTDDSSSTAYVQQLSLTSESDAVYYCARYYDDH 356  
DB 421 GLEWIGYINPARGYTNVQKFKDKATLTDDSSSTAYVQQLSLTSESDATYYCARYYDDH 480  
QY 357 YCLDYWGQGTTLTVSS 372  
DB 357 YCLDYWGQGTTLTVSS 372

DB 481 YCLDYWGQGTTLTVSS 496  
RESULT 15  
AD283625  
ID AD283625 standard; protein; 496 AA.  
XX  
XX AD283625;  
XX  
XX 14-JUL-2005 (first entry)  
DE CD3 specific binding construct SEQ ID NO 247.  
XX  
XX neoplasm; inflammation; immune disorder; infection; allergy;  
XX graft versus host disease; cytostatic; Antiinflammatory;  
XX immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
XX  
XX Synthetic.  
XX  
XX WO2005040220-A1.  
XX  
XX 06-MAY-2005.  
XX  
XX 15-OCT-2004; 2004WO-EP011646.  
XX  
XX 16-OCT-2003; 2003BP-00023581.  
XX  
XX (M1CR-) MICROMET AG.  
PA Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;  
PI Carr FU, Hamilton AA, Williams S;  
XX  
XX WPI; 2005-333494/34.  
DR N-PSDB; AD283624.  
XX  
XX New cytotoxically active CD3 specific binding construct comprises a first  
PT domain specifically binding to human CD3 and an Ig-derived second binding  
PT domain, useful for treating, preventing, or ameliorating, e.g.  
PT proliferative disease.  
XX  
XX Claim 20; SEQ ID NO 247; 639pp; English.  
XX  
XX The invention relates to a cytotoxically active CD3 specific binding  
CC construct comprising a first domain specifically binding to human CD3 and  
CC an Ig-derived second binding domain. The CD3 specific binding construct  
CC above or the construct produced by the process, nucleic acid molecule,  
CC vector, or host is useful for the preparation of a pharmaceutical  
CC composition for the prevention, treatment, or amelioration of a  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
CC construct is useful for treating, preventing, or ameliorating  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The present sequence represents the amino  
CC acid sequence of a CD3 specific binding construct.  
XX  
SQ Sequence 496 AA;

Query Match 89.0%; Score 1821; DB 9; Length 496;  
Best Local Similarity 70.4%; Pred. No. 1.5e-105;  
Matches 349; Conservative 11; Mismatches 12; Indels 124; Gaps 1;  
QY 1 ELVWTPGSSSLTVTAGKRVMSCKSSQSLNSGNQKXLYTWYQKPPQPKLLIYMASTR 60  
DB 1 ELVWTPGSSSLTVTAGKRVMSCKSSQSLNSGNQKXLYTWYQKPPQPKLLIYMASTR 60  
QY 61 ESVGPDFRTSGSGGTDFLTITSSVOAEDLAVYYCONDSYPLTFGAGTKLEIKGGGSGG 120  
DB 61 ESVGPDFRTSGSGGTDFLTITSSVOAEDLAVYYCONDSYPLTFGAGTKLEIKGGGSGG 120

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QY 121 GGS GGS E V O L L E O S G A E L V R P G T S V K I S C K A S G A F T N Y W L G W V K O R P G H G L E W I G D I 180
    |||||
Db 121 GGS GGS E V O L L E O S G A E L V R P G T S V K I S C K A S G A F T N Y W L G W V K O R P G H G L E W I G D I 180
    |||||
QY 181 F P G S G N I H Y N E K F K G K A T L T A D K S S T A Y M O L S L T F E D S A V Y F C A R L R N M D E P M D Y W G Q 240
    |||||
Db 181 F P G S G N I H Y N E K F K G K A T L T A D K S S T A Y M O L S L T F E D S A V Y F C A R L R N M D E P M D Y W G Q 240
    |||||
QY 241 G T T V T V S G G G S D I ----- 255
    |||||
Db 241 G T T V T V S G G G S D I V L T Q S P A T L S L S P E R A T L S C R A S Q S V S Y M W Y Q O K P K A P K R M I 300
    |||||
QY 256 ----- 255
    |||||
Db 301 Y D T S K V A S G V P A R F S G S G T D Y S L T I N S L E A E D A T Y Y C O Q M S N P L T F G G T R V E I K G 360
    |||||
QY 256 ----- K L O O S G A E L A R P G A S Y K M S C K T S G Y T F T R Y T M H W K O R P G Q 296
    |||||
Db 361 E G T S T G S G S G S G G A D V O L V O S G A E V K P G A S Y K V S C K A S G Y T F T R Y T M H W K O R A P G Q 420
    |||||
QY 297 G L E W I G Y I N P S R G Y T N Y N O K F K D K A T L T T D K S S T A Y M O L S L T S E D S A V Y Y C A R Y Y D D H 356
    |||||
Db 421 G L E W I G Y I N P S R G Y T N Y N A D S V K G R F T I T T D K S T A Y M E L S L R S E D T A T Y Y C A R Y Y D D H 480
    |||||
QY 357 Y C L D Y W G O G T T V T V S S 372
    |||||
Db 481 Y C L D Y W G O G T T V T V S S 496
    |||||

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Search completed: March 6, 2006, 14:46:23  
 Job time : 91 secs

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